Time Series Calibration (1990-2013) and Escapement Goal for Atnarko River Chinook Salmon

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TIME SERIES CALIBRATION (1990-2013) AND ESCAPEMENT GOAL FOR ATNARKO RIVER CHINOOK SALMON

by

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ABSTRACT

Vélez-Espino, L.A., Winther, I., Koroluk, B., and Mullins, G. 2014.Time series calibration (1990-2013) and escapement goal for Atnarko River Chinook salmon. Can. Tech. Rep. Fish. Aquat. Sci. 3085: vii + 90 p.

Chinook salmon (*Oncorhynchus tshawytscha*) escapement assessments have been conducted on the Atnarko and Bella Coola River systems in central British Columbia (BC) since 1950 using a variety of methods. Three methods have been used since 1990 to generate independent estimates of Chinook salmon escapement. These methods are based on (*i*) capture per unit effort (CPUE) during broodstock collection, (*ii*) carcass counts during dead pitching, and (*iii*) visual counts during drift-boat surveys. The average of these three population estimates (3MA method) has been used as the escapement estimation method for domestic purposes. Calibration of the time series of escapement from the 3MA estimates or its individual components was necessary to bring estimates within the Pacific Salmon Commission's (PSC) data standards. Mark-recapture programs conducted in the Atnarko River Chinook salmon from 2001 to 2003 and from 2009 to 2013 formed the basis of the calibration of the escapement time series. This report documents (i) the analyses of the mark-recapture data using maximum likelihood (ML) estimation within a model selection framework, (ii) the calibration of the 1990-2013 Atnarko Chinook escapement time series using Generalized Linear Models (GLM) based on the mark-recapture escapement estimates and the data routinely collected for the 3MA method, and (iii) the development of a habitat-based escapement goal for wild Atnarko Chinook. Using a watershed area of 1,035 km^2 in the habitat-based model for ocean-type Chinook, the spawning escapement at maximum sustainable yield (S_{msy}) was estimated to be 5,009 and the spawning escapement at replacement (S_{rep}) was estimated to be 14,595. The effects of barriers to fish passage in the habitat data sets were examined with respect to their effects on the watershed areas and the resulting effects on the escapement parameters. This habitat-based escapement goal represents a first iteration in the process of refinement required to quantify S_{msy} and S_{rep} for this stock. The estimation model used for time series calibration also serves to generate reliable escapement estimates based on two of the three components of the 3MA method: broodstock CPUE and carcass counts. The development of a calibrated time series of escapement and an escapement goal support the incorporation of Atnarko Chinook as an escapement indicator stock and an exploitation rate indicator stock in PSC assessments. The ability to produce robust and defensible escapement estimates from relatively simple and low cost methods has increased the probability that monitoring of Atnarko Chinook escapement will continue.

RÉSUMÉ

Vélez-Espino, L.A., Winther, I., Koroluk, B. et Mullins, G. 2014. Time series calibration (1990-2013) and escapement goal for Atnarko River Chinook salmon. Rapp. tech. can. sci. halieut. aquat. 3085: vii + 90 p.

Depuis 1950, on effectue des évaluations des échappées de saumon quinnat (*Oncorhynchus tshawytscha*) dans les réseaux hydrographiques des rivières Atnarko et Bella Coola dans le centre de la Colombie-Britannique à l'aide de diverses méthodes. Trois méthodes sont utilisées depuis 1990 pour générer des estimations indépendantes des échappées de saumon quinnat. Elles sont fondées sur (*i*) les captures par unité d'effort (CPUE) pendant la collecte de géniteurs, (*ii*) les dénombrements de carcasses pendant les examens des carcasses et (*iii*) les dénombrements visuels pendant les relevés à bord de bateaux dérivants. La moyenne de ces trois estimations de population (méthode 3MA) sert de méthode d'estimation de l'échappée à des fins nationales. Il était nécessaire de calibrer la série chronologique de données sur les échappées découlant des estimations 3MA ou ses différentes composantes afin de ramener les estimations à l'intérieur des normes de données de la Commission du saumon du Pacifique (CSP). Les programmes de marquage et recapture exécutés sur le saumon quinnat de la rivière Atnarko de 2001 à 2003 et de 2009 à 2013 constituent le fondement de la calibration de la série chronologique de données sur les échappées. Le présent rapport décrit (i) les analyses des données sur le marquage et la recapture à l'aide d'une estimation de la probabilité maximale (PM) par application d'un cadre de sélection de modèle; (ii) la calibration de la série chronologique des données sur les échappées de saumon quinnat dans la rivière Atnarko de 1990 à 2013 à l'aide de modèles linéaires généralisés (MLG) en fonction des estimations des échappées marquées et recapturées et des données recueillies régulièrement dans le cadre de la méthode 3MA; (iii) l'élaboration d'un objectif d'échappée fondé sur l'habitat pour le saumon quinnat sauvage de la rivière Atnarko. En appliquant le modèle fondé sur l'habitat pour le saumon quinnat de type océanique à une zone de 1 035 km^2 du bassin hydrographique, nous avons estimé que la production maximale soutenable de l'échappée de géniteurs (G_{pms}) était de 5 009 et que l'échappée de géniteurs au moment du remplacement (G_{remp}) était de 14 595. Les effets des obstacles au passage du poisson dans les ensembles de données sur l'habitat ont été examinés du point de vue de leurs effets sur les zones des bassins hydrographiques et des effets qui en résultent sur les paramètres des échappées. Cet objectif d'échappée fondé sur l'habitat représente une première occurrence dans le processus d'amélioration requis pour quantifier G_{pms} et G_{remp} pour ce stock. Le modèle d'estimation utilisé pour calibrer la série chronologique sert également à produire des estimations fiables sur les échappées en fonction de deux des trois composantes de la méthode 3MA : les CPUE du stock de géniteurs et le dénombrement des carcasses. L'élaboration d'une série chronologique calibrée de données sur les échappées et d'un objectif d'échappée appuie la désignation du saumon quinnat de la rivière Atnarko en tant que stock indicateur de l'échappée et que stock indicateur du taux d'exploitation dans le cadre des évaluations de la CSP. La capacité de produire des estimations fiables et défendables sur les échappées à l'aide de méthodes relativement simples et

peu coûteuses a augmenté la probabilité de poursuivre la surveillance des échappées de saumon quinnat dans la rivière Atnarko.

1.0. INTRODUCTION

The Coded Wire Tag (CWT) workgroup of the Pacific Salmon Commission (PSC) recently identified that some major Chinook salmon (*Oncorhynchus tshawytscha*) production regions and life histories were poorly represented by CWT indicator stocks currently used for assessments by the PSC (PSC 2008). A major production area identified without a CWT indicator stock was the central coast of British Columbia (BC). Chinook salmon abundance in the central coast is dominated by returns to the Atnarko River in the Bella Coola River watershed (Riddell 2004). Although marking with CWTs was initiated in 1976 for Atnarko Chinook salmon at the Snootli Hatchery (Bella Coola, BC), significant issues prevented the inclusion of this population as a CWT indicator stock for PSC assessments. The deficiencies included: (i) indeterminate quality for estimates of total escapement; (ii) inadequate sampling to allow for the estimation of freshwater CWT recoveries; (iii) data coordination and reporting problems; and, (iv) inadequate funds to conduct robust and effective sampling and analysis (PSC 2008). In response to the recommendations from the PSC CWT Workgroup, Vélez-Espino et al. (2011) completed the compilation, evaluation, and revision of Atnarko Chinook CWT recovery data from freshwater fisheries and escapement. These developments, allowed them to undertake cohort analyses for this population. The reconstruction of the exploitation and spawning history of Atnarko Chinook was a major accomplishment for the stock and provided an exploitation rate indicator where none had existed. The successful completion of cohort analyses for this stock not only provided key population statistics such as survival, maturation rates, and exploitation rates but also contributed to the goal of incorporating Atnarko Chinook into PSC assessments to better represent life histories and exploitation patterns of central BC Chinook salmon populations. 2012 was the first year Atnarko Chinook was included in the annual exploitation rate analysis conducted by the PSC (PSC 2012).

In response to the recommendations of the CWT workgroup (PSC 2008), Fisheries and Oceans Canada initiated a five-year mark-recapture program in the Atnarko River to improve escapement estimates for early summer Chinook in 2009 (Vélez-Espino et al. 2010). While the most thorough Chinook escapement assessments in central BC had come from the Bella Coola/Atnarko system (Riddell 2004), the need for validation of the quality of estimates of total escapement remained an issue. Estimates of Atnarko Chinook escapement have been produced since 1950 (BCWCS 2007; Vélez-Espino et al. 2011) and terminal run estimates in the Bella Coola River exist since 1980 (Pestal 2004, Riddell 2004, Vélez-Espino et al. 2011). However, the estimates have not been scrutinized or standardized across different enumeration and estimation methods. Mark-recapture experiments before 2009 were conducted sporadically: in 1984-1986 (Slaney 1986, Andrew et al. 1988) and again in 2001-2003 (Sturhahn 2009).

Three methods have been used since 1990 to generate independent estimates of Chinook salmon escapement. These methods were based on (*i*) capture per unit effort (CPUE) during broodstock collection, (*ii*) carcass counts during dead pitching, and (*iii*) the number of spawners

observed during drift-boat surveys. The average of three population estimates (hereafter called 3MA) was identified by Vélez-Espino et al. (2011) as a promising index of abundance. The simplicity and low cost of these three methods has allowed the continuous monitoring of Atnarko escapement. However, further calibration was required for the time series of escapement estimates derived from the 3MA method, or its individual components, to meet or exceed the PSC data standards and provide robust and defensible estimations of Atnarko Chinook spawning escapement. Increased efforts during the 2001-2003 and 2009-2013 mark-recapture experiments, and the application of modern capture-recapture analytical approaches, are expected to provide the necessary data to calibrate the time series of escapement produced by the 3MA method. An improved escapement time series is an important development that will improve planning of terminal fisheries, improve the accuracy of abundance indices and fishery planning for mixed-stocks fisheries in North/Central British Columbia and Southeast Alaska, and improve information to support First Nations Treaty negotiation.

The development of an escapement goal would launch Atnarko Chinook as an escapement indicator stock for the evaluation of BC Individual Stock-Based Management (ISBM)[2] fisheries under the Pacific Salmon Treaty (PST). Atnarko Chinook is one of the stocks listed in Attachment IV of the Chinook Chapter in the 2009 PST, representing North/Central BC Chinook for the evaluation of ISBM exploitation rate obligations. While North BC Chinook are represented by Kitsumkalum River Chinook, the Central BC group (currently represented by Wannock, Chuckwalla, and Dean Rivers), did not have an exploitation rate indicator for PSC assessments until the work by Vélez-Espino et al. (2011). In addition, differences in life history, ecology, and molecular genetics between Kitsumkalum Chinook and Atnarko Chinook place these stocks in separate conservation units in Canada (Holtby and Ciruna 2007). In terms of life history, Atnarko Chinook exhibits a life history type that is predominantly ocean-type (Pestal 2004) while Kitsumkalum Chinook is mostly stream type (McNicol 1999).

Escapement indicator stocks represent wild populations or the wild components of enhanced populations. The Atnarko River is an enhanced system, and the ability to track hatchery contributions to naturally spawning contingents is possible due to the successful recovery of CWTed fish in the spawning grounds (Vélez-Espino et al. 2011). A calibrated time series of escapement, the ability to produce escapement estimates in the future even in the absence of mark-recapture studies, and the development of an escapement goal could enable the full incorporation of Atnarko Chinook as both exploitation rate and escapement indicator stock for PSC assessments.

A Chinook salmon indicator program in the central coast has been perceived as feasible once funding was available for an escapement program in the Atnarko River (Riddell 2004). Atnarko Chinook are easily captured and recovered as this system is not as susceptible to fall

[2] ISBM management regimes apply to all Chinook salmon fisheries subject to the PST that are not abundance-based, mixed-stock ocean fisheries (i.e., AABM fisheries).

flooding as many other coastal Chinook systems (BCWCS 2007). The close proximity of qualified staff from the Snootli Hatchery reduces the risk inherent with conducting mark-recapture programs on remote systems. Given the history of mark-recapture programs on the Atnarko, the effort requirements for sufficient tag application and carcass recovery are well understood. Past mark recapture programs were successful in terms of tagging and tag-recovery rates that provided escapement estimates with relatively low coefficients of variation (Vélez-Espino et al. 2010).

Modern mark-recapture experiments rely on individual encounter histories and maximum likelihood estimators that are asymptotically unbiased, normally distributed, and of minimum variance (Cooch and White 2013). Model selection and a thorough and systematic evaluation of models fit to the data have become important aspects in the analysis of mark-recapture data (Lebreton et al. 1992). The accuracy of these methods for salmon escapement estimation are second only to passage counts that provide complete censuses of migrating salmon populations. This methodological rigor generates robust and defensible estimates of abundance (as well as other population attributes such as survival, capture probabilities, and entrance probabilities). The methods provide equal or greater accuracy and precision than the Petersen or other ad hoc estimators. Relevant assumptions associated with specific models are tested and the information generated by the experiment is used thoroughly, thus increasing confidence in the accuracy of estimated parameters. Ad hoc estimators have the disadvantage of being unable to untangle the components of return rates, which are the product of survival and capture rates (see Cooch and White 2013). It is also important to acknowledge that some modern mark-recapture models have the advantage of providing separate inferences about survival and capture rates.

The specific objectives of this investigation are: (1) to develop robust and defensible escapement estimates based on mark-recapture data and maximum likelihood (ML) estimation within a model selection framework; (2) to calibrate the 1990-2013 Atnarko Chinook escapement time series using Generalized Linear Models (GLM) based on these high-quality escapement estimates and data routinely collected for the 3MA; and, (3) to develop a habitat-based escapement goal for wild Atnarko Chinook and evaluate the 1990-2013 calibrated time series for wild Atnarko Chinook relative to this escapement goal. Our analyses entailed four steps. First, we follow the systematic approach for the analysis of mark-recapture data described in Vélez-Espino et al. (2010) to produce ML escapement estimates for 2001-2003 and 2009-2013. Second, we use GLMs to calibrate the historic (1990-2013) time series of escapement. These models are based on mean escapement estimates from mark-recapture studies as response variable and different combinations of broodstock CPUE, number of carcasses recovered, and run year as predictors. The best model, based on the Akaike Information Criteria (AIC) and analysis of deviance, is then used calibrate the escapement time series and to produce an escapement estimation model for years without mark-recapture studies. Third, we calculate an escapement goal for wild Atnarko Chinook based on allometric relationships between the wild spawners (excluding Jacks) required to produce maximum sustainable yield (S_{msy}) and watershed

area (Parken et al. 2006). Lastly, we evaluate the calibrated time series of escapement relative to the escapement goal. To do this, hatchery contribution in the escapement for each year in the time series is quantified based on Atnarko Chinook CWT release and recovery data.

2.0. METHODS

2.1. Mark-recapture escapement estimation

Individual encounter histories were constructed from mark-recapture experiments for 2001-2003 and 2009-2013 following the sampling and recording protocol described in Vélez-Espino et al. (2010). The main attributes of this protocol include: (1) double tagging (Kurl-lock Ketchum tags as primary individual marks and operculum punches as secondary marks); (2) spatial representation; (3) stratification by group (female, male or jack); (4) thorough recording of recaptures and losses on capture; (5) temporal stratification based on the distinction between the phases of the experiment (tagging, carcass recovery, and an overlapping period between tagging and recovery), environmental conditions, and field logistics; and (6) randomization procedures to treat lost primary tags (i.e., redistribution of primary tags at risk among recovered fish possessing only secondary marks). The generation of individual encounter histories (IEH), as opposed to summary statistics, allows many alternative analyses of mark-recapture data and allows detailed goodness-of-fit tests. An IEH is a contiguous series of specific dummy variables, each of which indicates something concerning the encounter of a given individual; for example, whether or not it was encountered on a particular occasion, how it was encountered (live or dead), where it was encountered, and so forth. The greatest advantage is that most modern mark-recapture techniques and software require this type of information. There is an explicit probability for every IEH, which include losses-on capture that represent individuals not released after an encounter either because they are dead or have been removed from the system (as in the case of broodstock removals). Vélez-Espino et al. (2010) provides a detailed description of the construction of IEH and how strata and covariates (if available) are incorporated in the encounter history.

The estimation of 2001-2003 and 2009-2013 Atnarko Chinook escapement estimates followed the systematic approach for the analysis of individual encounter histories described in Vélez-Espino et al. (2010), which was designed to provide precise and unbiased estimates of spawning escapement. The main attributes of this approach include: (i) testing for demographic closure; (iii) thoroughly evaluating the goodness-of-fit of model structures; and, (ii) allowing different hypotheses about the demographic and catchability attributes of the studied population to be expressed within a model selection framework characterized by the principles of parsimony and maximum likelihood.

2.1.1. Closure

Closure means that the size of a population is constant over the period of investigation: no additions (birth or immigration) or losses (death or emigration) occur. A closed population is one that does not change composition during the course of the study. This assumption is difficult to meet as it is rarely true in a biological population. Although there are no concerns about deaths in studies of Pacific salmon escapement because all fish die after spawning, unknown deaths (e.g., pre-spawning mortality) remain an issue as well as emigration outside of the study area or the entrance of new individuals into the system after the start of the study. The closure test for time-specific data developed by Stanley and Burnham (1999) was used to test the null hypothesis of closed-population model M_t against the open population Jolly-Seber model. The closed-population model M_t corresponds to a model where the probability of capture and recapture vary with time but the two are identical in any given sampling occasion. The closure test is a χ^2 test that can be used to determine the nature of closure violations, namely, unknown additions and/or losses to the population during the study period. Computer software Close Test Version 3 (T.R. Stanley and J.D. Richards, USGS, Fort Collins Center, Colorado) was used to test for closure. This software includes for comparison the closure test developed by Otis et al. (1978). The closure concept can be subdivided into two components: geographic and demographic. Geographic closure is due to a boundary limiting population dispersal whereas demographic closure refers to closure to additions and losses. This distinction is important because open models are open to demographic closure, but geographic closure can still be a critical assumption (White et al. 1982).

2.1.2. Model-structure types

Depending on the results of the closure test, two types of maximum likelihood model structures were used: Closed-population models or open population model POPAN. Both model-structure types enabled the construction and fit assessment of numerous sub-models based on different schemes for temporal and group stratification. The evaluation of closed-population models was separately conducted for maximum likelihood estimators developed by Otis et al. (1978) and the more recent approach developed by Huggins (1989). The reader is referred to Chao (2001) for a recent review and general theory. The main difference between these two approaches is that the Otis et al.'s model includes abundance in the likelihood whereas the Huggins' model leaves abundance condition out of the likelihood. The primary advantage of the Huggins' approach is that individual covariates can be used in the modelling. In the open-population case, robust estimators exist that compute both gross and net escapement in POPAN (Schwarz and Arnason 1996) based on a generalization of the Jolly-Seber model that uses a multinomial distribution from a super-population (i.e., the total number of animals that are ever available for capture in the population of interest over the course of the study). The POPAN system brings major advantages to mark-recapture studies of open populations, allowing the estimation of abundance

and entry rates in addition to survival and capture rates. These models are defined by their explicit assumptions about the main probability components of the likelihood estimation: capture (p), survival (φ), and recruitment/entrance to the study area (b). Hence, survival rates, capture rates, and immigration rates can change during the course of the study and can be also different between groups (e.g., females, males, and Jacks) and/or spatial strata (e.g., stream sections). This modelling framework facilitates the incorporation of constraints (e.g., equal survival per time period), is not affected by unequal time intervals between sampling occasions, and covariate data on any scale can be easily incorporated.

The algorithms for the abovementioned model-structure types have been described elsewhere (Schwarz and Arnason 1996, Chao 2001, Vélez-Espino et al. 2010, Cooch and White 2013) and are not further elaborated herein.

2.1.3. Model selection

Model selection should be oriented around satisfaction of as many model assumptions as practically possible so that a simple and reasonably efficient model can be used for estimation (Pollock et al. 1990). The goal of model selection is to identify a biologically meaningful model that explains the significant variability in the data but excludes unnecessary parameters (Burnham et al. 1987). Mark-recapture analyses of spawning escapement followed a model selection approach as described in Lebreton et al. (1992), which encompasses the following steps:

1) Start from a global model (i.e., the model with a parameter for each strata and process in the experiment) compatible with species biology and asses its fit

2) Use goodness-of-fit tests of the global model

3) Select a more parsimonious model using Akaike's Information Criterion (AIC) to limit the number of formal tests

4) Compare the parsimonious model with neighbouring models using likelihood ratio tests (LRT)

5) Obtain maximum likelihood estimates of model parameters, including precision

These steps were separately applied to both, open-population and closed models (depending on the results of the closure test) using Program MARK (Gary C. White, Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, Colorado; http://www.phidot.org/software/mark). Modern and robust analyses of mark-recapture data rely on maximum likelihood estimation requiring iterative numerical techniques for which computing power is necessary. Numerous software programs are currently available and among these,

Program MARK is the ultimate tool. MARK is the most comprehensive and widely used software application currently available for the analysis of data from marked individuals. MARK is a very flexible and powerful program, with many options, and technical and theoretical sophistication, enabling model selection and goodness of fit testing. It encompasses virtually all methods currently used for analysis of marked individuals - including many new approaches only recently described in the primary literature. MARK offers far more flexibility and power in statistical modeling and hypothesis testing than other widely available and frequently used programs. It also uses a consistent and familiar 'Windows interface', and allows the user to work with a consistent data format throughout the process.

Goodness of fit of the global model was evaluated using the computer program RELEASE (Gary C. White, Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, Colorado), which is integrated in MARK. This is a test for differences in survival and capture probabilities of individuals within each group (females, males, and Jacks) within sampling intervals and differences in survival and capture probabilities among groups. RELEASE relies in a series of χ^2 tests following the protocol provided by Burnham et al. (1987). In this protocol, TEST 1 is an omnibus test for a treatment effect(s) (i.e., significant differences between groups) that performs an overall test of equality of all survival and capture probabilities among groups. TEST 2 and TEST 3 together are useful to test two of the assumptions underlying most mark-recapture models: (i) every marked individual present in the population at time i has the same probability of recapture p_i; (ii) every marked individual in the population immediately after time i has the same probability of surviving to time i+1. TEST 2 assesses individual capture probabilities within a group or strata (e.g., females) while TEST 3 assesses individual survival probabilities within a group.

AIC was used for model selection because it provides reliable and objective basis for screening the set of possible models to select the best model and neighbouring competing models for further consideration. Additional tests such as the implementation of the likelihood-ratio test (LRT), which requires that one of the models be a special case (i.e., nested) of the more general model, were conducted using MARK applications to test for significant differences between models neighbouring the best model (the top ranked model with the lowest AIC). The difference in deviance between 'nested models' (models in which one model differs from another by the elimination of one or more model terms) is distributed as a χ^2 statistic with the degrees of freedom given as the difference in the number of estimable parameters between the two models. This forms the basis of the LRT and it is included herein to refine the results of the AIC model selection.

In addition, the stratified Petersen estimator (Robson and Regier 1964) was computed for comparison to the best ML models. Two-sample, pooled-Petersen and stratified-Petersen estimators are commonly applied to mark-recapture data from spawning escapement in Pacific salmon populations. The application of the Petersen estimator to mark-recapture data depends on

critical assumptions intrinsic to closed-population models originally designed for short-term studies where births, deaths, immigration, emigration, and changes to capture probabilities can be ignored (Pollock et al. 1990). These assumptions cannot be liberally ignored for long-term studies such as in mark-recapture escapement estimation of Pacific salmon, typically lasting around two months. Ad hoc estimators, like the Petersen, only estimate population size under very restrictive and, in many cases, unrealistic assumptions (Nichols and Pollock 1983).

2.2. GLM-based time series calibration (1990-2013)

The 1990-2013 time series of escapement abundance was calibrated through generalized linear models (GLM). In a GLM, each outcome of the dependent variable, **Y**, is assumed to be generated from a particular distribution in the exponential family, (e.g., normal, binomial, Poisson and gamma distributions), among others. The mean, $\boldsymbol{\mu}$, of the distribution depends on the independent variables, **X**, through:

$$\mathrm{E}(\mathbf{Y}) = \boldsymbol{\mu} = g^{-1}(\mathbf{X}\boldsymbol{\beta}) \tag{1}$$

where E(**Y**) is the expected value of **Y**, $\mathbf{X}\boldsymbol{\beta}$ is the linear predictor, a linear combination of unknown parameters, $\boldsymbol{\beta}$, and g is the link function. In this framework, the variance is typically a function, **V**, of the mean:

$$\mathrm{Var}(\mathbf{Y}) = \mathrm{V}(\boldsymbol{\mu}) = \mathrm{V}(g^{-1}(\mathbf{X}\boldsymbol{\beta})). \tag{2}$$

The unknown parameters, $\boldsymbol{\beta}$, were estimated through maximum likelihood using computer software JMP11 (2013 SAS Institute Inc.; http://www.jmp.com). The Poisson distribution was used to specify the conditional distribution of the response variable "total escapement" (N_y). The linear predictor component encompassing the linear function of predictors is:

$$\eta_i = \alpha + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_k X_{ik} \tag{3}$$

The Log link-function was used to transform the expectation of the response variable, $\mu_i \equiv \mathrm{E}(\mathrm{Y_i})$, to the linear predictor:

$$g(\mu_i) = \eta_i = \alpha + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_k X_{ik} \tag{4}$$

with predictor variables (i) number of carcasses recovered during deadpitching (CR), (ii) broodstock CPUE as average catch (broodstock retrieved) per net set (BS_CPUE), and (iii) run year (RY). Given the small number of points, overdispersion (the ratio of residual deviance to

degrees of freedom) was evidenced in all GLMs by the ratio of the Pearson-statistic to its degrees of freedom being greater than 2. Any level of dispersion >1 should be considered and modeled to prevent magnification of error rates and skewed confidence intervals McCullagh and Nelder (1989). Therefore, an overdispersion parameter was included[3].

The corrected Akaike's Information Criterion (AICc) was used to select the best model:

$$\text{AICc} = -2\ \text{loglikelihood} + 2k + 2k(k+1))/(n-k-1) \qquad (5)$$

where k is the number of estimated parameters in the model and n is the number of observations in the data set. This value may be compared with other models to determine the best-fitting model for the data. The model having the smallest value, as discussed in Burnham and Anderson (2002), is usually the preferred model. Changes in goodness-of-fit statistics are often used to evaluate the contribution of subsets of explanatory variables to a particular model. The deviance, defined to be twice the difference between the maximum attainable log likelihood and the log likelihood at the maximum likelihood estimates of the regression parameters, was also used as a measure of goodness of fit.

AIC differences (Δ_i) and Akaike weights (w_i) for model i were also computed because the "raw" AIC value is meaningless outside of the context of the other models under consideration. Akaike weights function as evidence ratios for interpreting results of multiple models (Burnham and Anderson 2002).

$$\Delta_i = \text{AIC}_i - \text{AIC}_{min} \qquad (6)$$

$$w_i = \frac{\exp(-0.5\Delta_i)}{\sum_{r=1}^{Z}\exp(-0.5\Delta_r)} \qquad (7)$$

where Z is the number of models being compared.

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[3]There is no exponential family corresponding to this specification, and the resulting GLM does not imply a specific probability distribution for the response variable. Rather, the model specifies the conditional mean and variance of Yi directly. Because the model does not give a probability distribution for Yi, it cannot be estimated by maximum likelihood. The usual procedure for maximum likelihood estimation of a GLM yields the so-called *quasi-likelihood* estimators of the regression coefficients, which share many of the properties of maximum-likelihood estimators. The quasi-likelihood estimates of the regression coefficients are identical to the ML estimates for the Poisson model. The estimated coefficient standard errors differ, however: If φ is the estimated dispersion for the model, then the coefficient standard errors for the *quasi-Poisson model* are $\varphi^{1/2}$ times those for the Poisson model. In the event of overdispersion, therefore, where $\varphi > 1$, the effect of introducing a dispersion parameter and obtaining quasi-likelihood estimates is (realistically) to deflate the coefficient standard errors.

2.2.1. Jacks

Since total escapement estimates of Atnarko Chinook derived from total-escapement GLMs include Jacks, the estimated number of Jacks was discounted from the total estimate to generate an adults-only estimate in years where mark-recapture studies took place (2001-2003 and 2009-2013). In years without mark-recapture data, the number of large males and females ($A_{3+,y}$) was estimated as the mean escapement estimate (N_y) minus the number of Jacks computed from the average proportion of Jacks in the escapement (p_j) estimated from mark-recapture studies, $A_{3+,y} = N_y (1- p_j)$. Alternatively, we also developed GLMs based on $A_{3+,y}$ as response variable and used AIC for model selection following the steps in the previous section.

2.3. Hatchery contribution

Hatchery releases of Chinook salmon in the Atnarko River has averaged around 2 million fry annually with ~10% marked with CWT's. This level of enhancement has occurred since the mid 1980's, usually splitting the release of juvenile fish between upper and lower Atnarko in an attempt to cover potential differences in outmigration timing between the areas. In addition, release timings are structured with yearling and sub-yearling smolt releases to match the various life history strategies present. Direct hatchery contributions are measured and compared using several methods. The annual Chinook deadpitch program is believed to be the least biased of the methods and historical mark presence data suggests an average hatchery contribution of approximately 35% of the spawning runs (Vélez-Espino et al. 2011). In some years, an estimated 30-40% of the total Chinook escapement to the Bella Coola watershed is of hatchery origin (Hilland and Lehman 2005).

The hatchery contribution to escapement was calculated by expanding the estimated number of CWT fish of each tag code group in proportion to the percentage of juvenile fish having a CWT at time of release:

$$EHC_{tc,y} = \frac{EST_{tc,y}(RM_{tc} + RUM_{tc})}{RM_{tc}} \qquad (8)$$

where $EHC_{tc,y}$ is the estimated hatchery contribution by tag code and recovery year, $EST_{tc,y}$ is the estimated number of CWT recoveries by recovery year for a single tag code, RM_{tc} is the number of Chinook released with CWTs for each tag code group, and RUM_{tc} is the number of Chinook released without CWTs for each tag code group. These estimates of hatchery contribution by tag code were then summed across all tag codes recovered in year y and divided by the mean escapement estimate in that year to determine the proportion of hatchery fish h_y:

$$h_y = \frac{\sum EHC_{tc,y}}{N_y} \qquad (9)$$

Lastly, the number of large wild Chinook by recovery year ($W_{3+,y}$) was computed as the product of large adults in the escapement and the complement of the hatchery proportion by year, $W_{3+,y} = A_{3+,y}(1 - h_y)$. Notice that the variable $W_{3+,y}$ is in the same units as the habitat-based escapement goal (next section).

2.4. Wild Chinook escapement goal

2.4.1. Watershed Area-Based Escapement Goal

The computation of a biologically-based escapement goal for Atnarko Chinook followed the method developed by Parken et al. (2006) and has been updated to include recent stock-recruitment data and stocks. The method relates productive capacity to watershed area based on results from a meta-analysis of 27 Chinook stocks distributed between central Alaska and northern Oregon, representing a broad range of environments and life histories. The resulting allometric models that predict S_{msy} and S_{rep} (spawners required to produced maximum sustained yield and replacement, respectively) from the watershed area adequately predicted these population parameters for seven case study examples. The S_{msy} generated through this method excludes Jack Chinook and is meant to represent only wild fish production. Following, we identify the sources of geographic data, describe a validation test to confirm our appropriate tracking of the methodology, and describe the application of this methodology to Atnarko Chinook.

2.4.2. Data Sources

The calculation of watershed area (for the Atnarko River) was performed using two Geographic Information System (GIS) data sets. The first was the Watershed Atlas (WSA) - BC WATERSHED GROUPS (1:50K). This data set was revised for the final time and published in 2005 and was the primary data source by Parken et al. (2006). The second data source was the Freshwater Atlas (FWA) of BC, which is derived from the Terrain Resource Information Management (TRIM) series of base maps (note FWA is based on TRIM not TRIM2 mapping, as TRIM2 had not been performed for the entire province at the time of writing). The TRIM set of data was at the 1:20K scale, and thus represented an increase in detail precision. The FWA also represented an increase in accuracy (with respect to geographic location) over the WSA as watershed GIS layers were computed directly from digital elevation contours for the FWA. As the regression parameters relating to spawners required for maximum sustainable yield and recruitment were computed in the original study using the WSA for BC rivers, this data was

considered more appropriate for the calculations performed in this study (however it should be noted that the stocks examined in tables 1 and 2 in Parken et al. (2006) include stocks from rivers in Alaska, Washington, Oregon, and Idaho, which use different GIS data sources). The program Quantum GIS (http://www.qgis.org/en/site/) was used to perform the majority of the GIS data manipulation after extracting BC river and watershed data available at https://apps.gov.bc.ca/pub/dwds/home.so.

Barriers to fish passage were found to be inconsistent between the FWA (Freshwater Atlas Obstructions layer) and other data compiled in the Provincial Obstacles to Fish Passage GIS Layer (which included data from the Fisheries Information Summary System (FISS), Fish Habitat Inventory and Information Program, the Field Data Information System, and inventory studies from the Resource Analysis Branch). When these layers were examined, the Provincial Obstacles to Fish Passage layer was more consistent with information from local fisheries experts.

2.4.3. Validation

Some validation was necessary to ensure that the methods in Parken et al. (2006) were applied correctly to the Atnarko watershed. The watershed areas of the Kitsault, Nicola, Nass, South Thompson and Wannock Rivers provided in Parken et al. (2006) were recalculated and these values were used in the allometric models to reproduce the results in the original study. Watershed areas were rounded to the nearest km^2. Differences between the values published by Parken et al. (2006) and the computed values were small and likely caused by rounding errors in all cases except for the Wannock River (Table 1).

The Wannock River watershed (Wannock Chinook stock unit, Owikeno Lake watershed) area was drawn from the WSA data. The stock is ocean-type with only two barriers to fish migration on streams of order 5 or higher, one on the Neechanz River and one on the Machmell River[4]. Despite the presence of some glacial coverage in the Wannock River watershed, no area was subtracted for non-hospitable sub basins from the WSA area in Parken et al. (2006). This fact was considered in the examination of the Atnarko watershed area. The area of the entire Wannock River watershed was confirmed as 3,935 km^2 using the WSA GIS data. Calculation of watershed area for the Neechanz River upstream of barrier with FISS Dataset ID 278937 is in agreement with the value 322 km^2 from the original study. However the furthest upstream barrier on the FISS system for the Machmell River is FISS Dataset ID 15927, which specifically comments "(10 TO 15 MILES UPSTREAM. FISH HAVE BEEN OBSERVED ABOVE. REF# = WL-006)". The watershed area upstream of FISS Dataset ID 15927 exceeds 600 km^2 and thus it is unlikely that this is the Machmell River barrier referred to in the original study. Therefore,

[4] Parken et al. (2006) list Machmell as a 5th order stream. The WSA lists it as 6th order stream. This had no impact on the results.

some other barrier must have been used upstream of FISS Dataset ID 15927, possibly near the confluence with Kilippi Creek, to achieve the given area in Parken et al. (2006).

2.4.4. Calculation of Watershed Areas, S_{msy} and S_{rep} for Atnarko watershed

The validation procedure confirmed that the method used to determine the habitat area for Atnarko was consistent with the method developed by Parken et al. (2006). The method entails eight steps described below for Atnarko Chinook.

1) Identify the stock unit: Atnarko River (Central BC) early summer Chinook (*Oncorhynchus tshawytscha*)

2) Identify the life history: predominantly ocean-type Chinook (Pestal 2004). However, the Atnarko falls geographically between the predominantly stream-type and ocean-type coastwide clusters and stream-type Chinook are present in the system `(Vélez-Espino et al. 2011).

3) Calculate the watershed area of stock:

a. WSA area 2,597 km^2 – value from WSA 6th order or higher watershed

b. FWA area 2,577 km^2 – value from FWA Watershed Groups layer

4) Calculate the area upstream of man-made barriers:

a. 0 km^2 upstream from man-made barriers on streams of 5^{th} order or higher (no dams, etc.).

5) Calculate the area upstream of natural barriers:

WSA areas upstream of barriers were calculated using the boundaries of watersheds with 3^{rd} order or higher streams. For barriers occurring within a watershed unit, interpretive boundary estimation was required and repetition of measurement ensured reliability to within an order of a few km^2. FWA areas upstream of barriers were calculated by combining assessment level watersheds. For barriers occurring within an assessment level watershed, the fundamental sub-watersheds were utilized. To demonstrate the effects of inclusion/ exclusion of areas upstream of natural barriers on both of the GIS data sets, the individual barriers are listed in Table 2 with their data source.

There were fundamental problems in stream order mismatch between the WSA and the FWA GIS data layers. In the Atnarko watershed, both Mosher Creek and Hunlen Creek appeared as watersheds with a maximum stream order of 3 in the WSA whereas they were both listed as order 5 in the FWA; this affected their respective inclusion / exclusion in the rest of the calculations. Thus, four area calculations were performed to investigate the choice of barriers in

the two data sets (Table 3): WSA FISS Only, WSA All Barriers, FWA FISS Only, and FWA All Barriers.

6) Calculate the area of inhospitable sub-basins:

There were 0 km^2 of glaciers (inhospitable sub-basins taken from FWA only in the case of glaciers) and no inhospitable sub-basins in 5^{th} order or higher stream systems in WSA; small and negligible areas on smaller order stream systems for Atnarko watershed (also much less than Wannock River system that was examined in the original study).

7) Subtract the areas of 4, 5, and 6 from 3:

Table 4 shows the Atnarko watershed areas after removing undesired areas.

8) Use the area from step 7 to calculate the desired stock recruitment parameters:

A visual representation of the watershed area calculations are given in Figure 1 (WSA) and Figure 2 (FWA).

2.5. Escapement trends of wild Atnarko Chinook

As a corollary to the present study, a formal evaluation of wild Atnarko Chinook escapement was conducted using four trend estimation methods: (1) log-linear regression of escapement against time (Eberhardt and Simmons 1992); (2) diffusion approximation (Dennis et al. 1991); (3) state-space exponential growth (Dennis et al. 2006) via maximum likelihood (ML; Humbert et al. 2009); and, (4) state-space exponential growth via restricted maximum likelihood (REML; Humbert et al. 2009). Method 1 assumed the variability in the data was purely governed by observation error and is hereafter referred to as exponential growth observation error model (EGOE). Method 2 ignored observation error and assumed variability in the data is entirely caused by environmental stochasticity and is hereafter referred to as exponential growth process noise model (EGPN). Methods 3 and 4 (exponential growth state-space, EGSS) assumed both observation error and process noise with the former using ML to derive parameter estimates and the latter using REML (Humbert et al. 2009).

3.0. RESULTS

3.1. Mark-recapture escapement estimation

The duration of the 2001-2003 and 2009-2013 mark-recapture studies of Atnarko River Chinook salmon ranged from 33 days (2010) to 60 days (2001) with the effective number of sampling days (tagging, recapturing, and deadpitching) ranging from 23 days (2010) to 40 days (2013).

Sampling days were grouped into temporal strata (occasions) that ranged in number from five in 2009 to 11 in 2010 (Table 5). The closure tests applied to individual encounter histories (IEHs) generated by these mark-recapture data were inconclusive for 2001-2003 and for 2013 (Appendix A), therefore supporting the development of closed population models for those years (Table 5). Best maximum likelihood (ML) closed population populations, as determined by their AICc ranking (Appendix B), were significantly different from the neighbour models (as per significant likelihood-ratio tests) and were characterized by time varying capture probabilities and differences between groups (females, males, and Jacks), except for 2001 when the best model did not include group-specific parameters for capture probabilities. The total number of parameters in the closed population models ranged from 10 (2001) to 27 (2013). Although the closure assumption was rejected for 2009, close-population models were developed for this year because there was considerable underreporting of recaptures during the tagging phase of the study (see Vélez-Espino et al. 2010). Open population models (POPAN) were therefore explored for years 2010-2012. In all cases, the best models were characterized by time varying entrance probabilities and differences between groups, thus reinforcing the rejection of closure as a suitable assumption (Table 5). The RELASE goodness-of-fit tests for POPAN models indicated there were significant differences in capture and/or survival probabilities between groups and not significant difference within groups, except for 2012 when the result of TEST2 +TEST 3 was significant thus suggesting that capture heterogeneity may have occurred this year (Tables 5, 6). Evidence of potential overdispersion (χ^2 statistic divided by the degrees of freedom > 1) existed only for 2011, indicating that the assumption of binomial variability underlying the structure of IEHs (Cooch and White 2013) may not be valid for that year. However, no c-hat (i.e., variance inflation factor) adjustment was considered necessary (see Table 6).

The number of IEHs ranged from 2,510 (2011) to 7,005 (2013). The mark-recapture study in 2011 was also characterized by the lowest number of carcasses examined (775) whereas the 2013 study had the largest number (5,186). The low numbers of both carcasses examined and IEHs in 2011 were partly due to extreme flood events that limited sampling activities. The lowest ML escapement estimate (7,425) occurred in 2012, followed by the largest escapement (22,690) in 2013. Escapement shows a general declining tendency from 2001 to 2012 followed by a large increase in 2013 (Table 7). Similar patterns in abundance were produced by the stratified Petersen estimates. However, coefficients of variation (CVs) were consistently lower for the best ML estimates of total abundance (females, males, and Jacks) and at the group level as well, except for jack CVs in years 2003, 2009, and 2011. The CVs for total abundance estimates from the best ML models ranged from 3.4% (2001) to 8.4% (2002) whereas those of the stratified Petersen estimator ranged from 5.6% (2001) to 13.5% (2011). Detailed results for ML model parameters other than abundance can be seen in Appendix C.

Although the assumption of closure was not categorically violated in four of the eight study years, the two-sample Petersen estimator pooled sampling occasions with significantly different capture or survival probabilities in seven of the eight study years. The best ML model

showed evidence of temporal changes in survival probabilities in all years except 2012. However, the closure assumption was clearly rejected in 2012. An evaluation of the relative error of the Petersen estimate of total abundance in relation to the best ML estimates indicated a clear negative relationship between the sampling rate (expressed as MR/N, where M is the number of tags applied, R is the number of tags recovered in the deadpitch, and N is the Petersen estimate) and the relative error in the Petersen estimate (Figure 3). When MR/N < 5 the error in the Petersen estimate was as large as ~40% whereas the error was relatively small when MR/N > 10. The error in the Petersen estimate was not directly related to the magnitude of the escapement.

3.2. Time-series calibration (1990-2013)

Seven GLMs were compared and ranked separately for total escapement (N_y) and large adults ($A_{3+,y}$) as response variables. In both cases, models including the number of carcasses recovered, broodstock CPUE, and run year ranked highest based on their AIC metrics and deviances (Table 8; Appendix D includes the data used in these models and details of the statistical analyses). Time series (1990-2013) of Atnarko Chinook total escapement and large adults in the escapement were calibrated using the best models in equations 10 and 11, where ε is a Poisson-distributed error term.

$$N_y = e^{[18.419389 + 0.0002274(CR) + 0.0143065(BS_CPUE) - 0.004878(RY)]} + \varepsilon \quad (10)$$

$$A_{3+,y} = e^{[36.554184 + 0.0002435(CR) + 0.0209815(BS_CPUE) - 0.014054(RY)]} + \varepsilon \quad (11)$$

Both calibrated time series produced escapement estimates similar to those produced using best ML models based on mark-recapture data for 2001-2001 and 2009-2013. The 95% confidence intervals estimates of both calibrated time series included, in all cases, the ML estimates (Figure 4). Nonetheless, the calibrated time series for total escapement performed better in terms of both smaller deviance and smaller parameter standard errors (Appendix D). The confidence intervals of the large-adult time series confidence interval was noticeably wider than that of the total escapement time series, particularly for the first 10 years (1990-2000) in the time series (Figure 4).

GLM calibrated time series of total escapement (i.e., including Jacks) based on Petersen estimates were also developed for comparison with those based on best ML estimates. The Petersen-based calibrated time series tracked the trends in the ML estimates well but showed a tendency to overestimate during the last decade and a tendency to underestimate during the first years of the time series (Figure 5). When the two calibrated time series were compared with the series generated by the 3MA method (1990-2008), the 3MA method performed relatively well from 2001 to 2008. This was unexpected given the assumptions involved in the 3MA method (see Vélez-Espino et al. 2011). However, the 3MA method underestimated escapement for the

first ten years of the time series with substantial differences from the best ML estimates from 1993 to 1997 (Figure 5).

3.2.1. Jacks

In addition to the lower statistical performance of the large-adult calibrated time series relative to the total escapement calibrated time series, the mean estimates for large adults in the escapement were counterintuitively greater than the estimates of total escapement for nine of the 24 years in the time series. This further supported the use of the total-escapement calibrated time series for subsequent analysis. Therefore, the estimated number of Jacks was subtracted from the total estimate to generate a large-adult estimate in years where mark-recapture studies took place (2001-2003 and 2009-2013). In years without mark-recapture data, the average proportion of Jacks in the escapement (p_j = 0.13; SE=0.04) estimated from mark-recapture studies was used to generate large-adult estimates.

3.2.2. Hatchery contribution

Hatchery contributions for the examined period (1990-2013) produced a proportion of hatchery fish averaging 34% (range: 13% -67%) in the escapement and 52% (range: 12% - 96%) in the broodstock with the percentage of hatchery fish consistently higher in the broodstock than in the escapement (except for 2008). This consistency suggests a possible positive selectivity of marked fish for hatchery purposes prior to 2008. The sharp decrease in hatchery contribution observed between 2006 and 2008 was associated to the absence of CWT releases for brood years 2003 and 2004 (Figure 6). CWT recoveries in the escapement from 1990 to 2013 included a negligible number of Jacks. Only 0.3% of the CWT recoveries observed in the escapement from 1990 through 2013 corresponded to age-2 fish. Therefore hatchery proportions (h_y) in Figure 6 represent large males and females only.

3.3. Escapement goal and wild Chinook escapement

Biologically-based escapement goals for PSC Chinook escapement indicator stocks are expressed as the number of wild, large spawners (excluding Jacks) associated with maximum sustainable yield (S_{msy}). When the watershed area estimates derived from the four different geographic data schemes in Table 4 were applied to the habitat-based model, the estimates for S_{msy} ranged between 4,187 and 7,087 and the estimates for S_{rep} ranged between 12,286 and 20,337 (Table 9). Substantial differences in S_{msy} and S_{rep} resulted from different criteria for the selection of GIS data sources (Table 9). The data scheme "WSA All Barriers", which is more

consistent with the method in Parken et al. (2006), produced an accessible Atnarko watershed area of 1,035 km^2. Using this watershed area value in the allometric model for ocean-type Chinook, the predominant life history type in the Atnarko, S_{msy} was estimated to be 5,009 spawners and S_{rep} was estimated to be 14,595. Alternatively, if the Atnarko River watershed area excludes those barriers to fish passage identified in FISS (increased GIS accuracy over the WSA), S_{msy} and S_{rep} would increase to 7,087 and 20,377, respectively. Hereafter we refer to these escapement goals as "lower" (5,009) and "upper" (7,087). These S_{msy}-derived escapement goals exclude the fish removed from the spawning grounds for hatchery purposes (i.e., broodstock).

3.4. Evaluation of large wild Chinook time series of escapement

Large wild Chinook salmon in the Atnarko River reached its highest abundance in 1992 with ~22,000 fish, following a precipitous decline with ~4,000 fish in 1997, thus below the lower escapement goal of 5,009 fish (Figure 7). The abundance of large wild Chinook bounced back to levels above the upper escapement goal, reaching 16,600 in 2001. After 2001, abundance declined through 2012 reaching its lowest level (~2,800) of the study period with about half the magnitude of the lower escapement goal. The number of large wild Chinook increased in 2013 to levels above the upper escapement goal with about 9,600 fish. Figure 7 also shows that in spite of time series calibration being based on total escapement (including Jacks and including hatchery and wild fish), the time series of large wild Chinook, generated in a posteriori fashion by subtracting Jacks and hatchery fish, represented well the ML-based estimated number of large wild Chinook derived from mark-recapture data in 2001-2003 and 2009-2013 (Figure 7).

Based on the 1990-2013 time series of escapement of wild Atnarko Chinook, the four trend estimation methods indicated a negative realized rate of change ranging from 0.9% (EGPN) to 3.6% (EGOE and EGSS-ML) annual decline (Table 10). The EGSS-REML model produced a mean annual rate of decline of 2.2%. Hindcasting of wild Chinook escapement by the two exponential growth state-space models showed the EGSS-REML outperformed the EGSS-ML model in terms of predicting the observed escapement (Figure 8). Staples et al. (2004) showed that REML are generally superior to ML estimates for the EGSS model. The EGSS-REML model also indicated that 62% of the variability in escapement was due to process noise and 38% due to observation (or sampling) error (Table 10). The 95% confidence interval for realized population growth was characterized by a 15.7% annual decline as lower limit and an 11.3% annual increase as upper limit. The estimated rate of decline for wild Chinook based on the entire time series would be dramatically increased if the assessment was based on the 2001-2013 time period.

4.0. DISCUSSION

4.1. Escapement estimation

Important developments in capture-recapture analysis have taken place in the last 25 years, and the analysis of mark-recapture data has evolved into a systematic approach that includes model selection (Lebreton et al. 1992). Model selection is important because data analysis in biological sciences should ideally be based on parsimonious models that provide an accurate approximation to the structural information in the data (Burnham and Anderson 2002). In general, bias decreases and variance increases with the number of model parameters. Hence, the fit of any model can be improved by increasing the number of parameters. On the one hand, overfitted models are often free of bias but have sampling variances that are unnecessarily large, thus rendering poor precision. On the other hand, underfitted models (i.e., ad hoc approaches) underestimate the sampling variance and ignore some important replicable structure in the data and therefore fail to identify effects that were actually supported by the data (Burnham and Anderson 2002). This often produces substantial bias in parameter estimators such as the stratified Petersen. Finding parsimonious models is thus important in order to achieve a proper trade-off between bias and precision.

Much attention has been paid to the achievement of precision standards escapement estimation in PST Chinook indicator stocks (e.g., CV of 15%). Precision of estimators should not be the only important criterion for estimation standards. Unless the underlying model is a reasonable approximation to the biology of the system, estimators may be extremely biased (Pollock et al. 1990). Accuracy (or its lack of thereof) is directly related to how modelling assumptions are met by escapement estimators. Thus, precision can be artificially increased by overlooking model assumptions while compromising accuracy. Accuracy in Chinook salmon escapement estimation should be of primary importance given the deterministic nature of the exploitation rate analysis conducted annually for Chinook stocks within the PST (PSC 2012), and given that escapement is assumed to be unbiased for the purpose of expanding observed (i.e., sampled) CWTed fish to total CWTed fish in the escapement (Pacific Salmon Commission Coded Wire Tag Workgroup 2008). The application of modern mark-recapture analytical techniques and model selection thus responds to these important concerns around the accuracy of escapement estimates and the biological realism of models.

Counterbalancing the difficulty in reflecting biological realism, study design should satisfy as many model assumptions as practically possible so that a simple and reasonably efficient model can be used for estimation (Pollock et al. 1990). The present investigation provides an example of the loss of accuracy in Petersen estimates as sampling rates decrease as well as an indication that greater precision in escapement estimates can be achieved by the best ML models in spite of their greater complexity and their having as many as 64 parameters (2010 best model). This shows the advantages of thoroughly assessing the fit of competing models

guided by the parsimony principle and the application of a systematic approach to the analysis of escapement data.

4.2. Time series calibration

The higher precision and tractable goodness-of-fit of best ML estimates made it important to calibrate the 1990-2013 time series of Atnarko Chinook escapement based on best ML models rather than the stratified Petersen estimates. This step was also relevant for the development of a reliable escapement estimation model that could be used for years without mark-recapture data. Table 11 shows 1990-2013 escapement time series that integrate the best calibrated estimates for years without mark-recapture data with the best ML estimates for years with mark-recapture data. This time series should be used in future analyses of Atnarko Chinook escapement until new data warrants new time series calibrations. The calibration of the time series and the estimation model developed herein can be updated every time new mark-recapture studies take place. The large overdispersion detected in all GLM models is expected to decrease as more data points are integrated into the analysis. Without the strong relationship between deadpitch carcass recoveries and total escapement, the performance of the GLMs with a limited sample size could have been inappropriate for time series calibration. As long as deadpitch carcass counts and broodstock CPUE data are available, the estimation model developed herein would serve as a powerful tool to generate defensible escapement estimates in the absence of mark-recapture data. Resources have been secured, through the PSC Northern Endowment Fund, to conduct a mark-recapture study of Atnarko Chinook in 2014. This information will enable the incorporation of additional data to the GLMs, which is expected to improve their overall performance and predictive capabilities.

4.3. Watershed Area-Based Escapement Goal

Linear regressions used to compute S_{msy} and S_{rep} (updated since Parken et al. 2006) are based on meta-analysis of the relationship between watershed area and the stock-recruitment reference points of 27 Chinook salmon stocks distributed between central Alaska and northern Oregon and representing a broad range of environments and life history. Using these allometric relationships to generate reference points for stocks and establish escapement goals without all necessary data for stock-recruitment analysis is extremely valuable since data typically needed for stock-recruitment analysis are expensive and difficult to gather. The habitat-based lower and upper escapement goals for Atnarko wild Chinook presented in this report represent a first iteration in the process of S_{msy} refinement for this stock. However, a stock-recruitment analysis of Atnarko Chinook could be undertaken in the future given the quantity and quality of data currently available for this stock:

a. Length of time series: *24 years (1990-2013)*
b. Estimation of large spawners in the escapement: *mark-recapture, index counts, and time series calibration; Jacks can be removed from the analysis*
c. Production: *cohort analysis based on CWT recoveries (Vélez-Espino et al. 2011)*
d. Escapement contrast - spawning abundance range > 4 (PSC 1999): *contrast = 6.8*
e. Hatchery contribution: *estimated annually*
f. Escapement CV: *mark-recapture CVs < 10%; calibrated time series CVs < 15%*
g. Production CV: *would require additional analytical procedures*
h. Age composition: *estimated annually from CWT and scale data*
i. Stray contribution: *quantified through cohort analysis; none in most years and negligible in few years*
j. Broodstock removal: *counted annually*
k. Pre-spawning mortality: *known for years with mark-recapture studies*

The main benefit of conducting a stock-recruitment analysis of Atnarko Chinook would be to eliminate the uncertainty in the S_{msy} estimate associated with the uncertainty in the watershed area and the effect of this uncertainty on the computation of a habitat-based escapement goal.

4.3.1. Uncertainty in watershed area

During this investigation, several observations were made with regards to calculation of watershed area. If only the FISS barriers to fish migration are considered, S_{msy} and S_{rep} are higher than when all barriers are used. Consideration of FISS barriers may be useful in general for standardization purposes given this system generates data that is more consistent with information from local fisheries experts. In addition, with systems such as the Atnarko River it is important to consider the dynamic change in obstruction conditions and the promptness of reporting of such changes to FISS or any other Fish Passage GIS layer. For instance, the flood event that occurred in 2010 significantly changed the location of many log jams from positions currently indicated in the FISS system. In remote watersheds it is possible that obstructions were not fully characterized by the data available in the Fish Passage GIS layers (e.g., Hotnarko River).

Although areas upstream of barriers were measured multiple times (creation of multiple watershed boundary polygons in the GIS program), the differences in repeated measurements were small and unbiased. However, it was demonstrated that a choice of inclusion/exclusion for various barriers and selection of GIS data source can result in large variations in the estimate of escapement goals. It was also noted that stream order miss-match was a fundamental problem between the two GIS data sets examined for the Atnarko system, which contributed to differences in area estimation resulting from the inclusion or exclusion of whole tributary stream systems from the calculations.

It may be worth re-examining BC stocks using the FWA because of a potential increase in both resolution and accuracy (FWA data is directly derived from digital elevation modelling of the TRIM data set for BC). Additionally, when TRIM2 mapping (TRIM2 is an improvement over TRIM mapping) is eventually completed for the province, it may again be pertinent to revisit watershed area for many BC Rivers.

Additional data, such as mean annual discharge and latitude were also calculated for the Atnarko River. Although mean annual discharge was eliminated from Parken et al. (2006) original analysis (due to unavailability of data) and watershed latitude was determined to be a less useful metric than watershed area, the following data are provided in case future refinement of the model warrants their inclusion.

a) Discharge Data

From 1973 to 2009 there was continuous discharge data for the Atnarko River at Environment Canada's Water Survey of Canada Hydrometric station 08FB006 (location is commonly known as "Flat Rock") and the mean annual discharge is calculated to be 27.2 m^3/s. The station was damaged in a 2010 flood event, and has been repaired in 2012. However new data should be recorded for at least 1 year to be added to the mean calculation. Although several flow monitoring stations have recorded discharge in the Bella Coola over the years, their locations have not usually been at the mouth of the river, and as such do not represent the complete discharge of the Bella Coola. The only data that exists from the mouth of the Bella Coola was recorded pre-1930, and is not usable due to discontinuous and short term monitoring.

b) Approximate Latitude of Atnarko River Watershed is 52.265 degrees north.

4.3.2. Uncertainty in escapement composition

An escapement goal based on wild Chinook does not automatically provide the complete knowledge about escapement composition required to manage terminal fisheries in enhanced systems. Although terminal fisheries occur mainly in the Bella Coola River and the vast majority of adult Chinook in the Bella Coola River are from the Atnarko River tributary (BCWCS 2007, Vélez-Espino et al. 2011), the challenge remains to determine in-season the hatchery contribution to the terminal run in any given year. While it is essential to develop escapement goals from the number of fish that spawn naturally (without help from hatcheries or channels) and based on the return of fish that have not been assisted by the hatchery, in practice, first generation hatchery Chinook salmon returning to the spawning grounds in the Atnarko River are expected to make the same contribution to recruitment as wild Chinook. Nonetheless, good management practices in enhanced systems should attempt meeting escapement goals while monitoring the abundance of wild Chinook to avoid the dampening of wild spawners. For example, Bella Coola/Atnarko fisheries management in a hypothetical year allows the

escapement of 8,000 adult Chinook (i.e., more than determined by the upper escapement goal). For hatchery purposes, 1,000 of these fish are collected as broodstock, and it is found after the analysis of adipose-fin-clip mark rates and estimated CWTs that only 3,500 of those adult Chinook were actually Atnarko wild Chinook spawners (i.e., less than the lower escapement goal for wild Chinook). Is this an indication that the escapement goal was not met? In this example, the escapement goal was met with a combination of 50% hatchery and 50% wild fish. However, the collection of broodstock needs to be considered separately to determine a management escapement goal ($EG_{management}$):

$$EG_{management} = EG_{wild\ \&\ hatchery} + Broodstock \quad (12)$$

Broodstock collected for hatchery purposes do not contribute to natural spawning and therefore should be considered as an add-on. In the Atnarko River, Chinook salmon broodstock are collected from the spawning grounds where the wild and hatchery components are mixed and for the last decade, the proportion of hatchery Chinook in the broodstock has been similar to the proportion of hatchery fish on the spawning grounds. Fishery management must also consider the hatchery component with respect to enhancement objectives designed to maintain healthy fish populations. Current guidelines for Canadian hatchery production recommend release targets and strategies should be set such that salmon returns of enhanced origin do not exceed 50% of the escapement goal and that broodstock collections do not exceed 33% of the returning stock.

4.4. Wild Chinook escapement trend

Escapement of large, wild Atnarko Chinook showed a clear tendency to decline from 2001 through 2012 to a level substantially below the lower escapement goal. This declining pattern was similar for the total adult escapement encompassing both hatchery and wild Chinook. Both total escapement and wild-only escapement were below the upper escapement goal in 2011 and below the lower escapement goal in 2012. This negative trend was relaxed in 2013 with the return to escapement levels above the upper goal. In spite of the inclusion of the large increase in escapement in 2013, the long-term (1990-2013) mean rate of change for Atnarko Chinook indicates a negative trend with a declining rate greater than 2% annually.

4.5. Final remarks

The calibration of the 1990 to 2013 time series of escapements for Atnarko Chinook makes an important contribution to our understanding of the status and trends in Central BC Chinook populations. Together with recent developments in CWT data and the ability to conduct cohort analyses, the escapement goal produced here allows for the evaluation of the performance of

domestic and international (PSC) fishery regimes on Central BC Chinook. This development is also an important first step for PSC assessments where the acceptance of escapement goals follows a rigorous Canada-U.S. bilateral process. Domestically, the habitat-based escapement goal for Atnarko Chinook is expected to guide commercial, recreational, and First Nations fishery plans in the Bella Coola and Atnarko rivers. Further, the development of methods to produce reliable escapement estimates in the absence of mark-recapture data ensures that future analyses are less hampered by funding constraints. While maintaining this ability depends on the existence of future mark-recapture programs to enable future time series calibrations and updated estimation models, these programs could be periodic and much less costly in the long term.

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6.0. TABLES

Table 1. Comparison between S_{msy} and S_{rep} calculated in this study and those in Parken et al. (2006) for six Chinook salmon stocks.

			Calculated		Parken et al. (2006)		Percentage Differences	
Stock Aggregate	Area [km^2]	Life History	S_{msy}	S_{rep}	S_{msy}	S_{rep}	S_{msy} diff	S_{rep} diff
Wannock	3173	Ocean	15399	42844	15300	42700	0.6%	0.3%
Kitsault	365	Stream	1273	3290	1300	3300	2.1%	0.3%
Nicola	7211	Stream	10035	26008	10000	26000	0.3%	0.0%
Nass	16615	Stream	17879	46380	17900	46400	0.1%	0.0%
S .Thompson	13494	Ocean	57823	152708	57600	152000	0.4%	0.5%

Table 2. Difference in areas upstream of natural barriers between GIS data sources WSA and FWA the effects of inclusion/exclusion of barriers. Dataset IDs A, B, and C correspond to noted barriers from FISS System whereas IDs D and E correspond to natural barriers to fish migration communicated by DFO personnel (personal communication; John Willis, Snootli Hatchery).

ID	FISS Dataset ID	Natural Barrier Description	Stream order WSA	WSA Area Upstream [km^2]	Stream Order FWA	FWA Area Upstream [km^2]
A	16890	Non- Specified Barrier (located on Upper Atnarko just above confluence of with south Atnarko River)	6	816	6	809.5
B	13134	Hunlen Falls (on Hunlen Creek)	3	NA	5	150.6
C	9692	Falls (on Young Creek)	5	251	5	244.5
ID	**Natural Barrier Description**		**Stream order WSA**	**WSA Area Upstream [km^2]**	**Stream Order FWA**	**FWA Area Upstream [km^2]**
D	Hotnarko River barrier (at Telegraph Creek)		5	495	5	483.4
E	Mosher Creek barrier (above highway)		3	NA	5	43.6

Table 3. Area removed above barriers under four different combinations of GIS data layers and barriers to fish migration identified in FISS and by DFO personnel.

Description	Barriers	Area Removed [km^2]
WSA FISS Only	A,C	1067
WSA All Barriers	A,C,D	1562
FWA FISS Only	A,B,C	1205
FWA All Barriers	A,B,C,D,E	1731

Table 4. Watershed areas used for calculations of Atnarko Chinook escapement goal for the four data schemes in Table 3.

Description	Barriers	Area Removed [km^2]	Area of Atnarko Watershed [km^2]
WSA FISS Only	A,C	1067	1530
WSA All Barriers	A,C,D	1562	1035
FWA FISS Only	A,B,C	1205	1372
FWA All Barriers	A,B,C,D,E	1731	846

Table 5. Sampling dimensions, output of closure tests, RELEASE goodness of fit significance, number of parameters, and likelihood ratio tests (LRT) for best ML models.

Year	Sampling Dimensions Duration d/Sampling days/Occasions	Closure Test	Goodness-of-Fit (Full Model) *f* TEST 1	TEST 2 + TEST 3	Best Model	Number of Parameters	LRT *d* (closest neighbour)
2001	60/33/7	Inconclusive	NA	NA	{p(t)=c(t)}	10	NA
2002	47/34/7	Inconclusive	NA	NA	{p(g,t)=c(g,t)}	24	Significant
2003	53/36/5	Inconclusive	NA	NA	{p(g,t)=c(g,t)}	18	Significant
2009	47/33/5	Additions *a*	Significant	Not significant	{p(g,t)=c(g,t)} *a*	18	Significant
2010	33/23/11	Additions	Significant	Not significant	{p(*), s(g,t), b(g,t)}	64	NA
2011	45/35/7	Additions	Significant	Significant *b, c*	{p(g), s(g,t), b(g,t)}	42	NA
2012	46/35/7	Additions	Significant	Not significant *b*	{p(g), s(*), b(g,t)}	25	NA
2013	53/40/8	Inconclusive	NA	NA	{p(g,t)=c(g,t)}	27	Significant

Table 6. Results of RELEASE Tests and whether lack of fit justified c-hat adjustment for full models.

Year	TEST 1	TEST 2 + TEST 3	Lack of fit c-hat adjustment
2001	NA	NA	NA
2002	NA	NA	NA
2003	NA	NA	NA
2009	Chi-square=52.82 (df=12) P=0.0000	Chi-square=19.66 (df=20) P=0.4793	No
2010	Chi-square=63.72 (df=26) P=0.0001	Chi-square=69.35 (df=70) P=0.499	No
2011	Chi-square=31.17 (df=11) P=0.0010	Chi-square=27.13 (df=9) P=0.0013 *b, c*	No *e*
2012	Chi-square=42.77 (df=17) P=0.0005	Chi-square=14.14 (df=14) P=0.4392 *b*	No
2013	NA	NA	No

a Problems with underreporting of recaptures the first year of the Atnarko program overestimated entrance probabilities using POPAN. A closed-population model was used instead. The best open-population model for 2009 was {p(g),s(*),b(g, t)}.
b TEST 2 statistics only. Too many unidentifiable parameters in the global model prevented the successful performance of TEST 3.
c There is evidence for heterogeneity in capture probabilities within groups; this may be linked to the observed overdispersion.
d Applies to nested models only. "NA" for non-nested models and POPAN models.
e Although there is evidence for overdispersion, c-hat was not adjusted because there was appropriate AIC ranking of biologically meaningful models.
f RELEASE only applicable to CJS open-population models.

Note 1: the global model is the fully stratified model with parameters for each group and time interval (also known as the full model). The test RELEASE in MARK uses this model by default.

Note 2: Only the component for "additions" in the Closure test is used since the component for "deaths and emigration" are irrelevant for salmon. The alternative answer for this column would be "No additions" or "Inconclusive"

Note 3: If $p<0.05$ in TEST 1, survival or/and capture probabilities are different among groups (female, male, jack)

Note 4: If $p> 0.05$ in TEST 2+TEST 3, there is no evidence for capture or survival heterogeneity within groups.

Note 5: Model description uses the parameters p = capture probability, c = recapture probability, s = survival probability, and b = entrance probability, and the strata g= group specific, t=time specific, and *=time and group invariant or time, group and reach invariant

Table 7. Mark-recapture data and summary statistics for Atnarko Chinook escapement estimation through best maximum likelihood models and stratified Petersen for years 2001-2003 and 2009-2013.

ATNARKO CHINOOK						Best Model					Stratified Petersen				
Year	Sex	Tags Applied	Tags Recovered	Carcasses Examined	Number of Encounter Histories [a]	Estimate [b]	95% lower limit	95% upper limit	Group %	CV	Estimate	95% lower limit	95% upper limit	Group %	CV
2001	F	562	131	2361	3121	10823	9832	11956	50.0%	5.0%	10074	8500	11937	48.5%	8.4%
	M	751	154	2054	2974	10106	9177	11167	46.7%	5.0%	9970	8523	11661	48.0%	7.7%
	J	39	7	144	198	706	608	826	3.3%	7.9%	725	377	1526	3.5%	32.4%
	Total	1352	292	4559	6293	21635	19617	23949		3.4%	20769	17400	25125		5.6%
2002	F	229	33	1262	1640	6520	5226	8273	56.6%	11.8%	8544	6141	12257	52.2%	16.7%
	M	268	36	839	1246	3907	3280	4721	33.9%	9.3%	6107	4448	8657	37.3%	15.9%
	J	43	2	115	160	1084	533	2441	9.4%	41.5%	1701	622	4253	10.4%	49.3%
	Total	540	71	2216	3046	11511	9039	15435		8.4%	16352	11212	25168		11.7%
2003	F	399	82	1215	2110	4981	4313	5789	39.5%	7.5%	5860	4732	7249	43.6%	10.5%
	M	470	63	837	1743	6944	6080	7966	55.0%	6.9%	6167	4837	7863	45.9%	11.9%
	J	76	3	72	144	694	305	1722	5.5%	47.6%	1405	574	3513	10.5%	43.5%
	Total	945	148	2124	3997	12619	10699	15477		5.5%	13433	10142	18625		8.5%
2009 [c]	F	289	106	1325	2017	4202	3748	4776	38.5%	6.2%	3594	2976	4338	33.4%	7.3%
	M	513	90	997	1807	4714	4233	5291	43.1%	5.7%	5637	4596	6911	52.4%	9.0%
	J	123	24	302	449	2009	1451	2879	18.4%	17.8%	1533	1047	2336	14.2%	16.8%
	Total	925	220	2624	4273	10926	9432	12946		4.7%	10764	8619	13586		5.8%
2010	F	271	43	604	1591	4711	4301	5184	44.9%	4.8%	3740	2793	4999	33.9%	13.1%
	M	616	38	344	1475	4605	4187	5089	43.9%	5.0%	5458	4004	7422	49.5%	14.4%
	J	120	4	75	238	1180	1000	1403	11.2%	8.7%	1839	814	3624	16.7%	38.6%
	Total	1007	85	1023	3304	10497	9488	11675		5.9%	11037	7611	16045		11.0%
2011	F	310	45	481	1270	4321	3673	5145	50.0%	8.6%	3259	2449	4329	34.1%	12.8%
	M	452	20	270	1139	3761	3143	4568	43.5%	9.6%	5846	3848	8808	61.2%	20.0%
	J	71	3	24	101	563	235	1697	6.5%	57.5%	450	153	500	4.7%	39.8%
	Total	833	68	775	2510	8645	7051	11409		7.1%	9555	6450	13637		13.5%
2012	F	233	20	306	1012	2559	2072	3047	34.5%	9.7%	3421	2252	5154	32.9%	19.6%
	M	140	23	404	761	2063	1697	2428	27.8%	9.0%	2379	1608	3500	22.9%	17.7%
	J	271	22	387	797	2803	2177	3429	37.8%	11.4%	4589	3075	6800	44.2%	18.9%
	Total	644	65	1097	2570	7425	5947	8904		6.0%	10389	6935	15454		11.9%
2013	F	391	64	2603	3388	11529	10000	13413	50.8%	7.5%	15704	12491	20367	55.5%	12.2%
	M	571	117	1929	2796	8433	7534	9502	37.2%	5.9%	9356	7874	11308	33.0%	8.9%
	J	148	29	654	821	2728	2167	3525	12.0%	12.5%	3253	2343	4835	11.5%	17.5%
	Total	1110	210	5186	7005	22690	19701	26440		4.7%	28313	22707	36510		8.1%

a The difference between the number of encounter histories and encounters (the sum of tagged fish and carcasses recovered minus tags recovered) is due to live recaptures that were not subsequently recovered in the deadpitch; live recapture data is not used in the Petersen estimator.

b Gross escapement estimate is used for comparison with Petersen in all cases when POPAN was used.

c Problems with underreporting of recaptures the first year of the Atnarko program overestimated entrance probabilities using POPAN. A closed-population model was used instead. The best open-population model for 2009 was {p(g),s(*),b(g,t)}.

Note 1: Confidence limits for the Petersen estimator were generated based on a Poisson distribution (Ricker 1975).

Table 8. GLM ranking through AICc and deviance model selection. The various models are combinations of predictors run year (RY), broodstock CPUE (BS_CPUE), and carcass recoveries (CR) for total escapement (N; includes Jacks) and adult escapement (A; excludes Jacks).

Model	AICc	ΔAICc	AICc weight	Deviance
N(CR, BS_CPUE, RY)	612.78	0.00	1	501.40
N(CR, BS_CPUE)	658.39	45.61	1.25E-10	556.35
N(CR, RY)	1044.28	431.50	2.00E-94	942.24
N(CR)	1236.26	623.48	4.10E-136	1139.82
N(BS_CPUE, RY)	14509.92	13897.14	0	14407.88
N(BS_CPUE)	14935.64	14322.86	0	14839.20
N(RY)	15431.03	14818.25	0	15334.59
A(CR, BS_CPUE, RY)	1721.61	0.00	1	1611.41
A(CR, BS_CPUE)	2123.96	402.35	4.27E-88	2023.10
A(CR, RY)	2528.54	806.93	5.99E-176	2427.68
A(CR)	3403.92	1682.31	0	3308.66
A(BS_CPUE, RY)	15611.96	13890.35	0	15511.09
A(BS_CPUE)	16867.31	15145.70	0	16772.04
A(RY)	16955.12	15233.51	0	16859.86

Table 9. S_{msy} and S_{rep} estimated by applying the regression parameters for ocean-type Chinook in Parken et al. (2006)[5] to watershed areas in Table 4. The results for the "WSA All Barriers" data scheme (highlighted) were most similar to that described in Parken et al. (2006).

Description	Barriers	Area Removed	Remaining Area of Atnarko Watershed [km^2]	S_{msy} (Ocean-type)	S_{rep} (Ocean-type)
WSA FISS Only	A,C	1067	1530	7087	20377
WSA All Barriers	A,C,D	1562	1035	5009	14595
FWA FISS Only	A,B,C	1205	1372	6433	18566
FWA All Barriers	A,B,C,D,E	1731	846	4170	12246

[5] Updated allometric regressions (Parken et al. 2006) to estimate the average S_{msy} (y) and S_{rep} (z) from watershed area (x) for ocean-type Chinook: $(\ln y) = 2.35 + (0.888 * \ln x)$; $(\ln z) = 3.67 + (0.852 * \ln x)$.

Table 10. Parameter estimates for exponential growth models with observation error (EGOE), process noise (EGPN), maximum-likelihood state-space (EGSS-ML), and restricted maximum-likelihood state-space (EGSS-REML) to estimate escapement trends for Atnarko River wild Chinook salmon. Model parameters are log-mean annual rate of change (μ), process noise variance (σ^2), observation error (τ^2), and log-abundance at time zero (x_0).

	μ	σ^2	τ^2	x_0
EGOE	-0.0355	0.0000	0.1736	9.4180
EGPN	-0.0085	0.2319	0.0000	9.3613
EGSS-ML	-0.0355	2.29e-10	0.1591	9.4179
EGSS-REML*	-0.0223	0.1052	0.0633	9.3658

* 95% confidence interval for EGSS-REML μ is: -0.1574 – 0.1128.

Table 11. Time series of Atnarko Chinook escapement integrating the calibrated values from best GLMs and the best ML estimates for years with mark-recapture studies (bold italic values). Time series are shown for "total escapement" including hatchery and wild females (F), males (M), and Jacks (J), "large adult escapement" including hatchery and wild F and M, and "large wild escapement" including only wild F and M.

Run Year	FMJ Hatchery + Wild	FM Hatchery + Wild	FM Wild
1990	16710	14537	11630
1991	13906	12098	8952
1992	32862	28590	22015
1993	35430	30824	20961
1994	28178	24514	12257
1995	23420	20376	8150
1996	20767	18067	5962
1997	11251	9788	4013
1998	13470	11719	6094
1999	16549	14398	7199
2000	17352	15096	9964
2001	***21635***	***20929***	***16743***
2002	***11511***	***10427***	***8550***
2003	***12619***	***11925***	***10136***
2004	11825	10287	8230
2005	11677	10159	7619
2006	19288	16781	9565
2007	8229	7160	5799
2008	7288	6341	5517
2009	***10926***	***8917***	***6331***
2010	***10497***	***9317***	***5683***
2011	***8645***	***8082***	***6061***
2012	***7425***	***4622***	***2542***
2013	***22690***	***19962***	***9860***

8.0 FIGURES

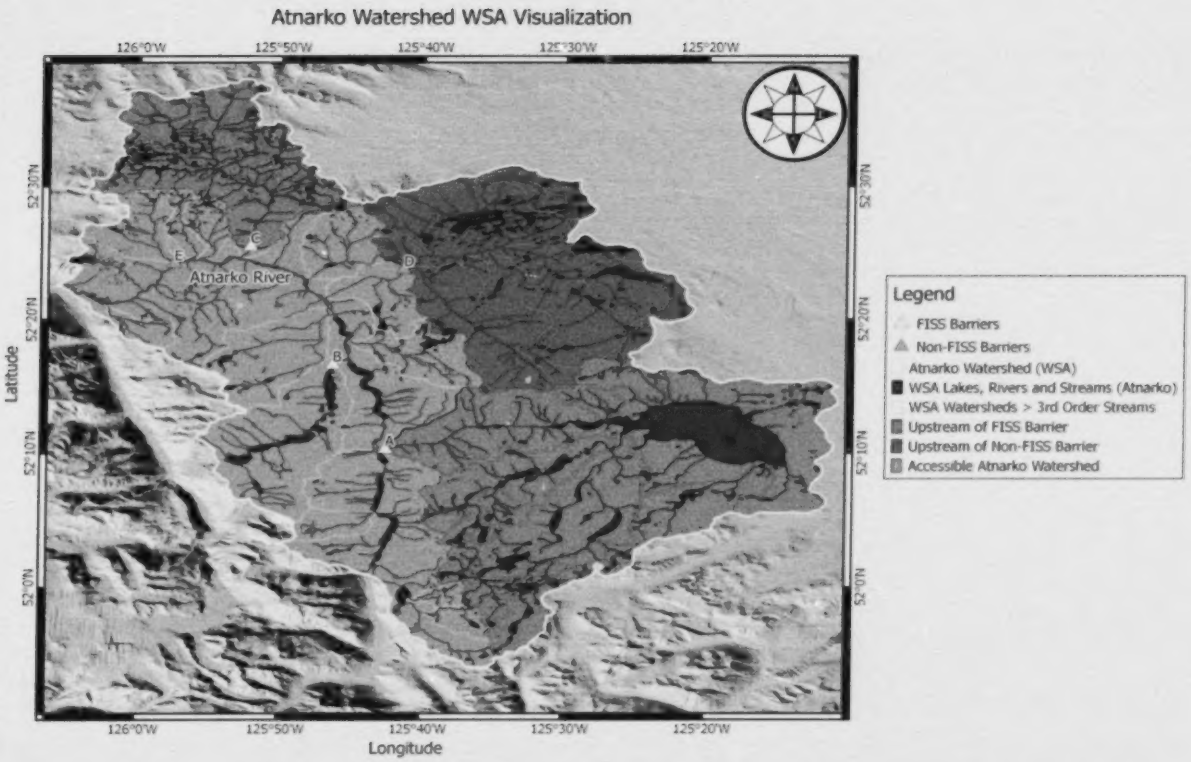


Figure 1. A representation of the WSA watershed area calculations for the Atnarko River watershed (coordinate reference system is NAD83).

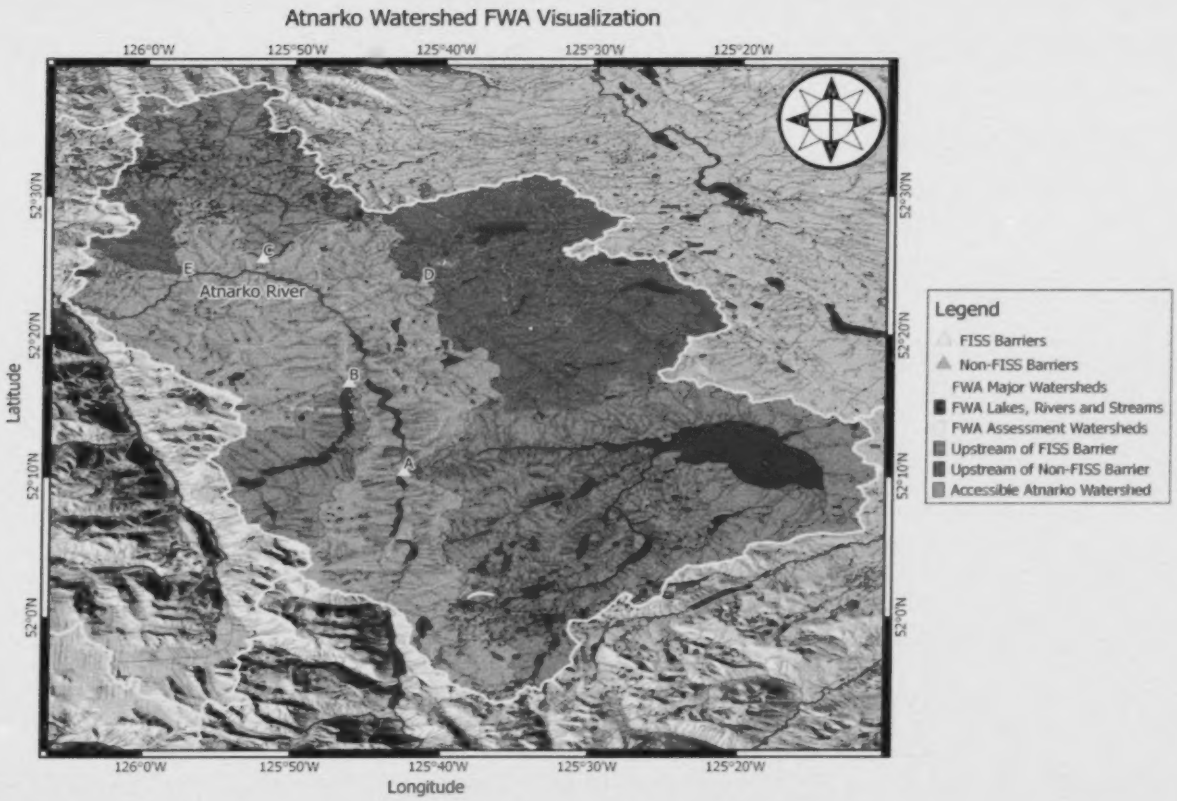


Figure 2. A representation of the FWA watershed area calculations for the Atnarko River watershed (coordinate reference system is NAD83).

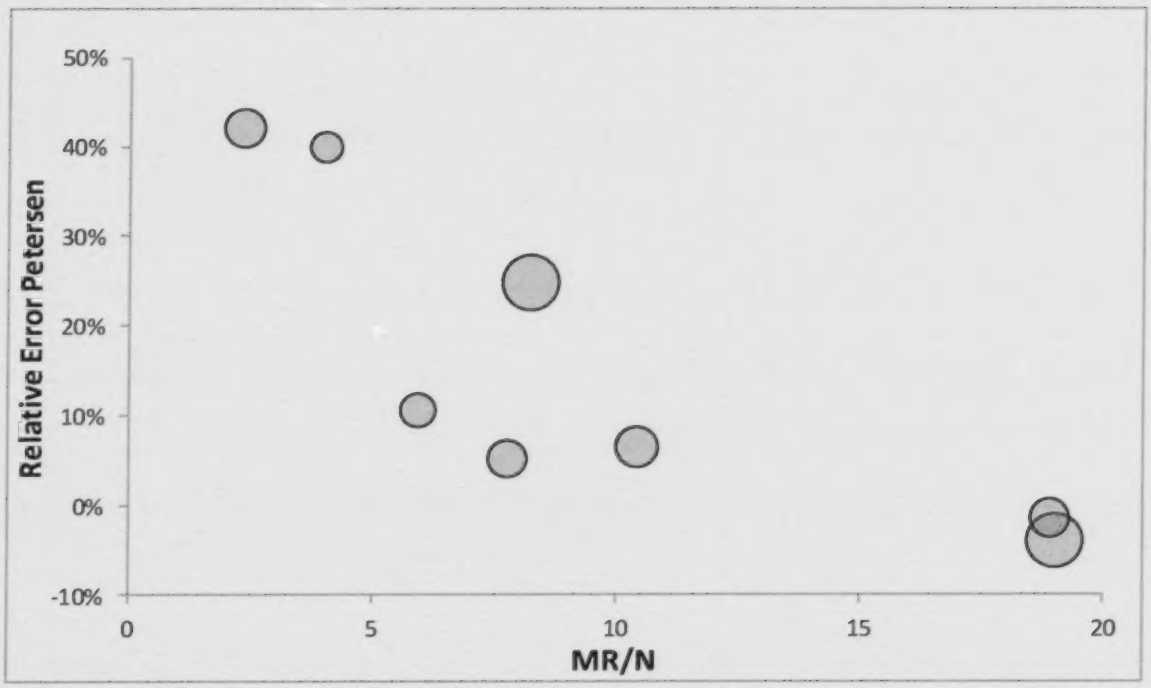


Figure 3. Relationship between sampling rate (marked * deadpitch recovered /Petersen escapement estimate) and the relative error of the Petersen estimate [(Best ML N - Petersen N)/Petersen N] from 2001-2003 and 2009-2013 studies. The area of the circles represents the relative magnitude of the best ML escapement estimate.

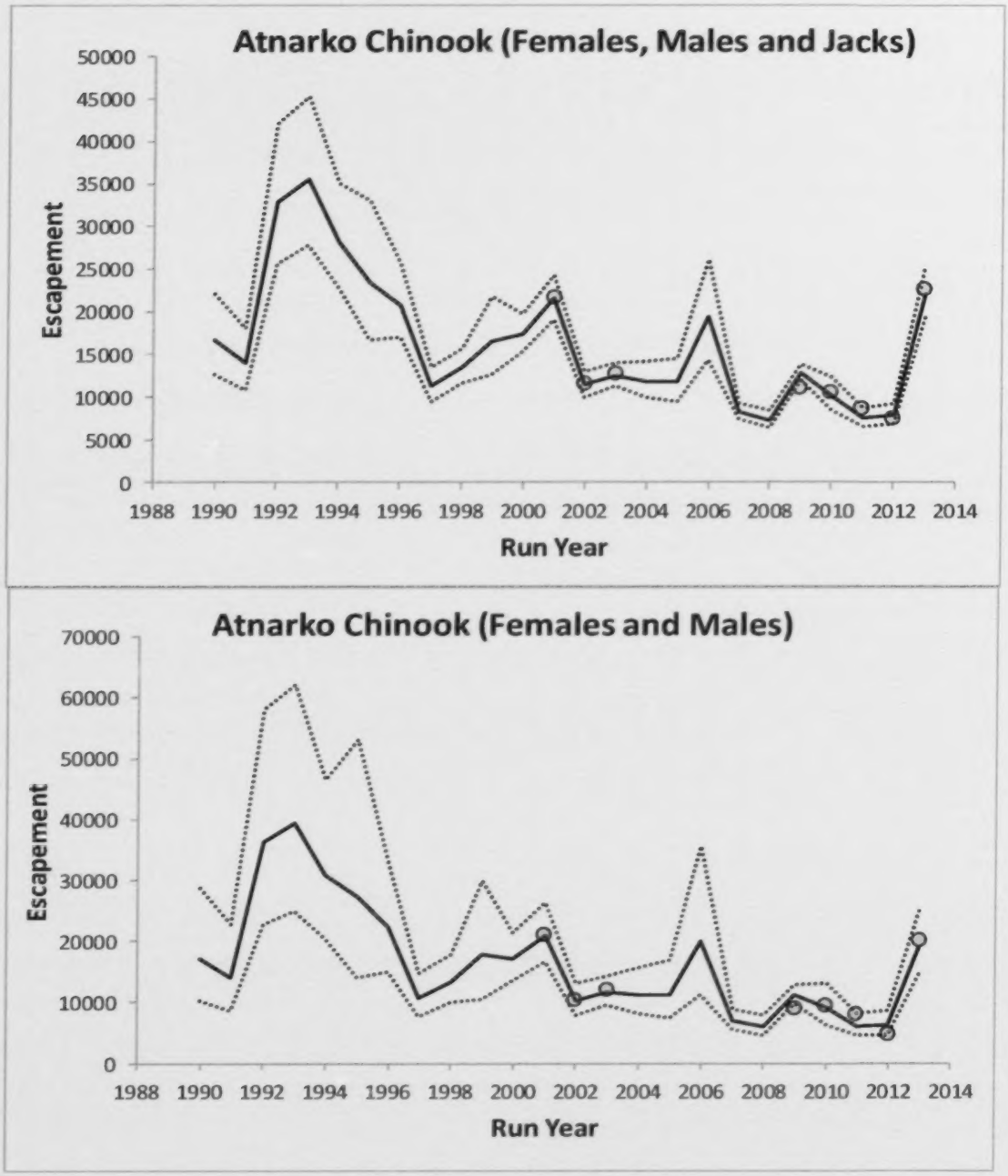


Figure 4. Calibrated 1990-2013 time series of Atnarko Chinook escapement. Solid line indicates the mean and dotted lines indicate the 95% confidence limits. Circles represent the mean escapement estimated from mark-recapture data using the best ML models. The upper panel includes Jacks in the escapement and the lower panel excludes Jacks from the escapement.

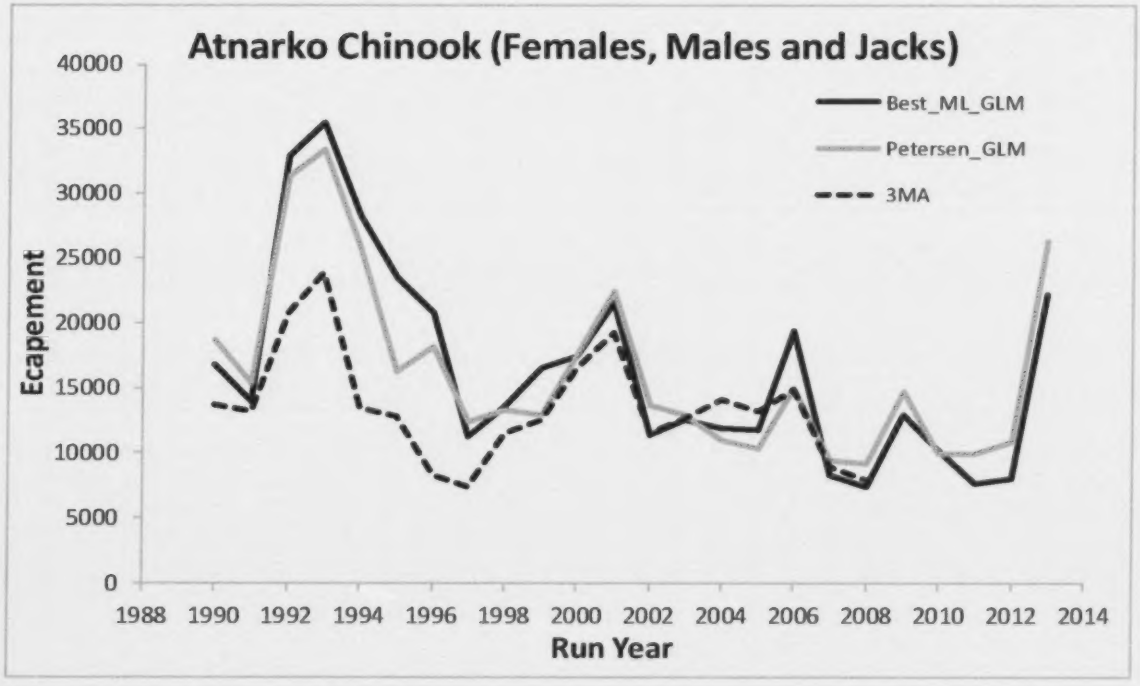


Figure 5. Comparing 1990-2013 calibrated time series derived from best ML models and Petersen estimates to the time series produced by the three-method average (3MA). The 3MA time series ends in 2008.

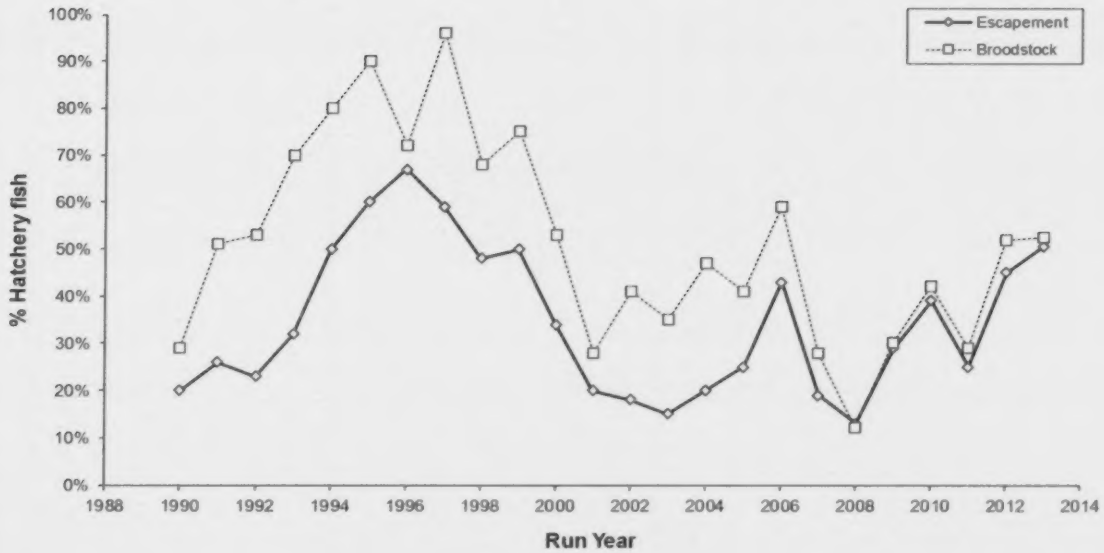


Figure 6. Hatchery contributions to Atnarko Chinook escapement and broodstock (1990-2013).

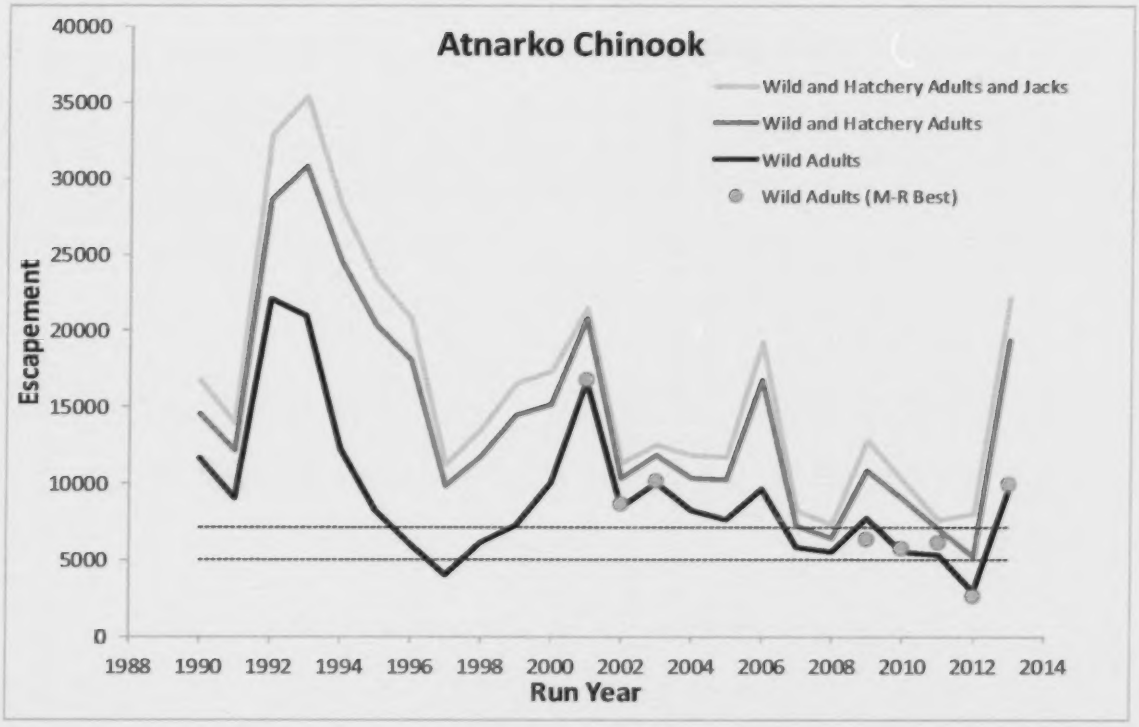


Figure 7. Calibrated time series of Atnarko Chinook escapement (1990-2013). Solid circles represent the number of wild adults estimated from the best ML model for years with mark-recapture (M-R) data. The dashed horizontal lines represent low (WSA All Barriers) and high (WSA FISS only) escapement goals.

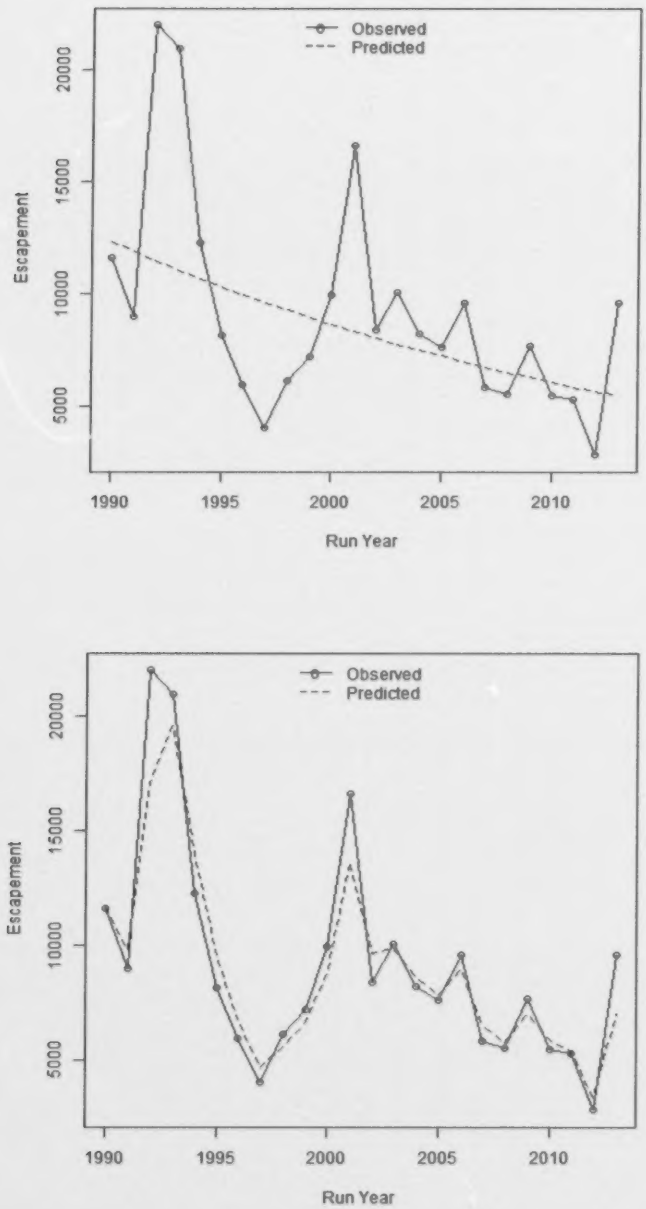


Figure 8. Wild Chinook observed escapement and predicted escapement from exponential growth state-space models of stochastic population growth using maximum likelihood (Top) and restricted maximum likelihood (Bottom).

9.0. APPENDICES

9.1. Appendix A

Results of Tests for closure for Atnarko Chinook escapement (2001-2003 and 2009-2013)

Glossary of terms used in the outcome of the closure test.

Chi-square statistic - This is equivalent to in Stanley and Burnham (1999), and is the test statistic for the overall closure test presented in that paper. Extreme values of this statistic result in low *p*-values, and suggests the population is not closed.

M_t - This is equivalent to M_t in Otis et al. (1978), and represents the closed-population capture-recapture model allowing for time variation in capture probabilities.

M_t vs *NM* - This component test evaluates whether there is evidence of additions to the population. It tests the fit of the closed-population model M_t (H_0: M_t) against the No-mortality model (H_a: *NM*) as a specific alternative.

M_t vs *NR* - This component test evaluates whether there is evidence of losses from the population. It tests the fit of the closed-population model M_t (H_0: M_t) against the No-recruitment model (H_a: *NR*) as a specific alternative.

NM vs *JS* - This component test evaluates whether there is evidence of losses from the population. It tests the fit of the No-mortality model (H_0: *NM*) against the Jolly-Seber model (H_a: *JS*) as a specific alternative.

NR vs *JS* - This component test evaluates whether there is evidence of additions to the population. It tests the fit of the No-recruitment model (H_0: *NR*) against the Jolly-Seber model (H_a: *JS*) as a specific alternative.

z-value - The computed value of the closure test statistic described in Otis, et al. (1978). Extreme values of this statistic result in low *p*-values, and suggests the population is not closed.

2001

Stanley & Burnham Closure Test (Low p-values suggest population not closed):
Chi-square statistic= 272.07799
df= 10.
p-value= 0.00000

Otis et al. (1978) Closure Test (Low p-values suggest population not closed):
z-value= 1.63285
p-value= 0.94875

Component Statistics of Stanley & Burnham Closure Test

Component	Chi-square	df	p-value
Tests for additions to population (Low p-values suggest there were additions)			
NR vs JS	29.13314	5.	0.00002
M_t vs NM	102.83582	5.	0.00000
Tests for losses from population (Low p-values suggest there were losses)			
M_t vs NR	242.94485	5.	0.00000
NM vs JS	169.24217	5.	0.00000

Note 1. Test was considered inconclusive when there was disagreement between the Stanley & Burnham and Otis tests.

2002

Stanley & Burnham Closure Test (Low p-values suggest population not closed):
Chi-square statistic= 394.22358
df= 10.
p-value= 0.00000

Otis et al. (1978) Closure Test (Low p-values suggest population not closed):
z-value= 2.06387
p-value= 0.98049

Component Statistics of Stanley & Burnham Closure Test

Component	Chi-square	df	p-value
Tests for additions to population (Low p-values suggest there were additions)			
NR vs JS	213.22612	5.	0.00000
M_t vs NM	332.29803	5.	0.00000
Tests for losses from population (Low p-values suggest there were losses)			
M_t vs NR	180.99745	5.	0.00000
NM vs JS	61.92555	5.	0.00000

Note 1. Test was considered inconclusive when there was disagreement between the Stanley & Burnham and Otis tests.

2003

Stanley & Burnham Closure Test (Low p-values suggest population not closed):
Chi-square statistic= 406.54368
df= 6.
p-value= 0.00000

Otis et al. (1978) Closure Test (Low p-values suggest population not closed):
z-value= 1.41238
p-value= 0.92108

Component Statistics of Stanley & Burnham Closure Test

Component	Chi-square	df	p-value
Tests for additions to population (Low p-values suggest there were additions)			
NR vs JS	27.25052	3.	0.00001
M_t vs NM	110.93943	3.	0.00000
Tests for losses from population (Low p-values suggest there were losses)			
M_t vs NR	379.29316	3.	0.00000
NM vs JS	295.60425	3.	0.00000

Note 1. Test was considered inconclusive when there was disagreement between the Stanley & Burnham and Otis tests.

2009

Stanley & Burnham Closure Test (Low p-values suggest population not closed):
Chi-square statistic= 718.33630
df= 43.
p-value= 0.00000

Otis et al. (1978) Closure Test (Low p-values suggest population not closed):
z-value= -3.74503
p-value= 0.00009

Component Statistics of Stanley & Burnham Closure Test

Component	Chi-square	df	p-value
Tests for additions to population (Low p-values suggest there were additions)			
NR vs JS	574.25259	12	0.00000
M_t vs NM	673.93006	23	0.00000
Tests for losses from population (Low p-values suggest there were losses)			
M_t vs NR	144.08371	31	0.00000
NM vs JS	44.40624	20	0.00133

2010

Stanley & Burnham Closure Test (Low p-values suggest population not closed):

Chi-square statistic= 388.48619
df= 18.
p-value= 0.00000

Otis et al. (1978) Closure Test (Low p-values suggest population not closed):

z-value= -1.50605
p-value= 0.06603

Component Statistics of Stanley & Burnham Closure Test

Component	Chi-square	df	p-value
Tests for additions to population (Low p-values suggest there were additions)			
NR vs JS	251.98030	9	0.00000
M_t vs NM	332.81853	9	0.00000
Tests for losses from population (Low p-values suggest there were losses)			
M_t vs NR	136.50589	9	0.00000
NM vs JS	55.66765	9	0.00000

2011

Stanley & Burnham Closure Test (Low p-values suggest population not closed):
Chi-square statistic= 127.88300
df= 10.
p-value= 0.00000

Otis et al. (1978) Closure Test (Low p-values suggest population not closed):
z-value= -6.61533
p-value= 0.00000

Component Statistics of Stanley & Burnham Closure Test

Component	Chi-square	df	p-value
Tests for additions to population (Low p-values suggest there were additions)			
NR vs JS	57.66430	5.	0.00000
M_t vs NM	103.99763	7.	0.00000
Tests for losses from population (Low p-values suggest there were losses)			
M_t vs NR	70.21869	5.	0.00000
NM vs JS	23.88536	3.	0.00003

2012

Stanley & Burnham Closure Test (Low p-values suggest population not closed):
Chi-square statistic= 116.86178
df= 9.
p-value= 0.00000

Otis et al. (1978) Closure Test (Low p-values suggest population not closed):
z-value= -3.55314
p-value= 0.00019

Component Statistics of Stanley & Burnham Closure Test

Component	Chi-square	df	p-value
Tests for additions to population (Low p-values suggest there were additions)			
NR vs JS	33.44719	4.	0.00000
M_t vs NM	85.98975	5.	0.00000
Tests for losses from population (Low p-values suggest there were losses)			
M_t vs NR	83.41459	5.	0.00000
NM vs JS	30.87202	4.	0.00000

2013

Stanley & Burnham Closure Test (Low p-values suggest population not closed):
Chi-square statistic= 1906.04009
df= 12.
p-value= 0.00000

Otis et al. (1978) Closure Test (Low p-values suggest population not closed):
z-value= -0.78554
p-value= 0.21607

Component Statistics of Stanley & Burnham Closure Test

Component	Chi-square	df	p-value
Tests for additions to population (Low p-values suggest there were additions)			
NR vs JS	1204.42636	6.	0.00000
M_t vs NM	1631.93649	6.	0.00000
Tests for losses from population (Low p-values suggest there were losses)			
M_t vs NR	701.61374	6.	0.00000
NM vs JS	274.10360	6.	0.00000

Note 1. Test was considered inconclusive when there was disagreement between the Stanley & Burnham and Otis tests.

9.2. Appendix B

Maximum Likelihood Model Selection for Atnarko Chinook Escapement (2001-2003 and 2009-2013)

Closed-population models are defined by the probability of capture (p) and the probability of recapture (c) under time-specific (t), group-specific (g), time- and group-specific (g,t), and/or invariant (*) conditions. Note: Model {p(t)=c(t)} corresponds to the M_t model used in the closure test.

Open population models (POPAN) are defined by the probability of capture (p), the probability of survival (s), and the probability of entering the system (b) under time-specific (t), group-specific (g), time- and group-specific (g,t), and/or invariant (*) conditions.

2001

Model	AICc	Delta AICc	AICc Weight	Model Likelihood	#Par	Deviance
{p(t)=c(t)}	-59074.124	0.00	1.000	1.000	10	5374.797
{p(g)=c(g)}	-52721.495	6352.6	0.000	0.000	6	11735.430
{p(*)=c(*)}	-52105.062	6969.0	0.000	0.000	4	12355.863
{p(g,t)=c(g,t)}	48.034	59122.0	0.000	0.000	24	64468.927

Note 1: Model {p(*),c(*)} did not converge
Note 2: Likelihood Ratio Test not applicable because the best models are not nested

2002

Model	AICc	Delta AICc	AICc Weight	Model Likelihood	#Par	Deviance
{p(g,t)=c(g,t)}	-25026.958	0.00	1.000	1.000	24	2629.131
{p(t)=c(t)}	-24608.576	418.38	0.000	0.000	9	3077.569
{p(g)=c(g)}	-22864.343	2162.6	0.000	0.000	6	4827.808

Note 1: Models {p(*)=c(*)} and {p(*),c(*)} did not converge

Likelihood Ratio test

Reduced Model	General Model	Chi-sq.	df	Prob.
{p(t)=c(t)}	{p(g,t)=c(g,t)}	448.438	15	<.0001
{p(g)=c(g)}	{p(g,t)=c(g,t)}	2198.676	18	<.0001
{p(g)=c(g)}	{p(t)=c(t)}	1750.238	3	<.0001

2003

Model	AICc	Delta AICc	AICc Weight	Model Likelihood	#Par	Deviance
{p(g,t)=c(g,t)}	-57343.530	0.00	1.000	1.000	18	3960.619
{p(t)=c(t)}	-56862.487	481.04	0.000	0.000	8	4461.685
{p(*),c(*)}	-54386.334	2957.2	0.000	0.000	5	6943.842
{p(g)=c(g)}	-54258.913	3084.6	0.000	0.000	6	7069.262
{p(*)=c(*)}	-54257.378	3086.1	0.000	0.000	4	7074.798

Likelihood Ratio test

Reduced Model	General Model	Chi-sq.	df	Prob.
{p(t)=c(t)}	{p(g,t)=c(g,t)}	501.065	10	<.0001

2009

Model	AICc	Delta AICc	AICc Weight	Model Likelihood	#Par	Deviance
{p(g,t)=c(g,t)}	-41213.207	0.00	1.000	1.000	18	2804.539
{p(t)=c(t)}	-41112.490	100.72	0.000	0.000	8	2925.284
{p(*),c(*)}	-38797.718	2415.4	0.000	0.000	5	5246.059
{p(g)=c(g)}	-38155.270	3057.9	0.000	0.000	6	5886.507
{p(*)=c(*)}	-38137.503	3075.7	0.000	0.000	4	5908.276

Likelihood Ratio test

Reduced Model	General Model	Chi-sq.	df	Prob.
{p(t)=c(t)}	{p(g,t)=c(g,t)}	120.745	10	<.0001

2010

Model	AICc	Delta AICc	AICc Weight	Model Likelihood	#Par	Deviance
{p(*),s(g,t),b(g,t)}	3681.265	0.00	1.000	1.000	62	NA
{p(*),s(g),b(g,t)}	3715.899	34.63	0.000	0.000	35	NA
{p(*),s(*),b(g,t)}	3764.147	82.88	0.000	0.000	33	NA
{p(g),s(g t),b(g,t)}	3809.012	127.75	0.000	0.000	64	NA
{p(*),s(t),b(g,t)}	3932.034	250.77	0.000	0.000	42	NA
{p(*),s(*),b(*)}	405367.889	401686	0.000	0.000	4	NA
{p(*),s(*),b(g)}	405371.921	401690	0.000	0.000	6	NA

Note 1: Deviance cannot be estimated in POPAN because population size cannot be estimated under the full model.

Likelihood Ratio test

Reduced Model	General Model	Chi-sq.	df	Prob.
{p(*),s(g),b(g,t)}	{p(*),s(g,t),b(g,t)}	0.000	27	******
{p(*),s(*),b(g,t)}	{p(*),s(g,t),b(g,t)}	0.000	29	******
{p(*),s(*),b(g,t)}	{p(*),s(g),b(g,t)}	0.000	2	******

Note 1: Since LRTs compare deviances of nested models to conduct significance tests of various factors in the models, and deviances cannot be estimated in POPAN, LRTs are inconclusive.

2011

Model	AICc	Delta AICc	AICc Weight	Model Likelihood	#Par	Deviance
{p(g),s(g,t),b(g,t)}	1610.618	0.00	1.0000	1.0000	42	NA
{p(g,t),s(g,t),b(g,t)}	1625.631	15.01	0.0006	0.0006	60	NA
{p(g),s(g),b(g,t)}	1826.442	215.82	0.0000	0.0000	27	NA
{p(g),s(g t),b(t)}	1904.287	293.67	0.0000	0.0000	30	NA
{p(*),s(g,t),b(g,t)}	1934.658	324.04	0.0000	0.0000	40	NA

Note 1: Deviance cannot be estimated in POPAN because population size cannot be estimated under the full model.

Likelihood Ratio test

Reduced Model	General Model	Chi-sq.	df	Prob.
{p(g),s(g t),b(g t)}	{p(g t),s(g t),b(g t)}	0.000	18	******

Note 1: Since LRTs compare deviances of nested models to conduct significance tests of various factors in the models, and deviances cannot be estimated in POPAN, LRTs are inconclusive.

2012

Model	AICc	Delta AICc	AICc Weight	Model Likelihood	#Par	Deviance
{p(g), s(*), b(g,t)}	1654.3165	0	0.4763	1	25	NA
{p(*), s(g), b(g,t)}	1655.9759	1.6594	0.20775	0.4362	25	NA
{p(*), s(*), b(g,t)}	1656.0448	1.7283	0.20072	0.4214	23	NA
{p(g), s(g), b(g,t)}	1657.1592	2.8427	0.11497	0.2414	27	NA
{p(g), s(*), b(t)}	1669.5658	15.2493	0.00023	0.0005	13	NA
{p(g), s(g), b(t)}	1673.6966	19.3801	0.00003	0.0001	15	NA
{p(*), s(*), b(t)}	1678.4234	24.1069	0	0	11	NA
{p(*), s(g), b(t)}	1681.8491	27.5326	0	0	13	NA
{[p(g), s(g,t), b(g,t)}	1828.1473	173.8308	0	0	42	NA
{p(*), s(g,t), b(g,t)}	1831.9375	177.621	0	0	40	NA
{p(g), s(t), b(g,t)}	1843.9251	189.6086	0	0	30	NA
{p(*), s(t), b(g,t)}	1851.4539	197.1374	0	0	28	NA
{p(g), s(t), b(t)}	1856.5456	202.2291	0	0	13	NA
{p(*), s(g,t), b(t)}	1863.5868	209.2703	0	0	28	NA
{p(*), s(t), b(t)}	1873.4922	219.1757	0	0	16	NA

Note 1: Models {p(g), s(g), b(g)}, {p(g), s(*), b(g)}, {p(g), s(*), b(*)},{p(g), s(t), b(*)},{p(g), s(g), b(*)},{p(*), s(*), b(*)},{p(*), s(*), b(g)}, {p(*), s(g), b(g)}, p(*), s(t), b(g)} and did not converge.

Note 2: Deviance cannot be estimated in POPAN because population size cannot be estimated under the full model.

Likelihood Ratio test

Reduced Model	General Model	Chi-sq.	df	Prob.
{p(g), s(*), b(g,t)}	{p(*), s(g), b(g,t)}	0.000	0	******
{p(*), s(*), b(g,t)}	{p(g), s(*), b(g,t)}	0.000	2	******
{p(*), s(*), b(g,t)}	{p(*), s(g), b(g,t)}	0.000	2	******

Note 1: Since LRTs compare deviances of nested models to conduct significance tests of various factors in the models, and deviances cannot be estimated in POPAN, LRTs are inconclusive.

2013

Model	AICc	Delta AICc	AICc Weight	Model Likelihood	#Par	Deviance
{p(g,t)=c(g,t)}	-69717.841	0.00	1.000	1.000	27	5970.590
{p(t)=c(t)}	-69506.009	211.83	0.000	0.000	11	6214.449
{p(g)=c(g)}	-64293.808	5424.0	0.000	0.000	6	11436.654
{p(*)=c(*)}	-64271.171	5446.6	0.000	0.000	4	11463.292

Note 1: Model {p(*),c(*)} did not converge

Likelihood Ratio test

Reduced Model	General Model	Chi-sq.	df	Prob.
p(t)=c(t)}	{p(g't)=c(g,t)}	243.859	16	<.0001
{p(g)=c(g)}	{p(g,t)=c(g,t)}	5466.064	21	<.0001

9.3. Appendix C

Best-model parameter estimates for Atnarko Chinook escapement (2001-2003 and 2009-2013)

In closed-population models, real-function abundance parameters are identical to estimates of derived abundance parameters.

In POPAN, real function abundance parameters represent the net escapement whereas the abundance estimates of derived parameters represent the gross escapement (i.e., superpopulation).

Spawning escapement estimates (N) are shown in the last three rows of the tables. Subscripts f, m, and j indicate female, male, and jack, respectively.

2001 Real Function Parameters of best model {p(t)=c(t)}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.0201067	0.0013668	0.0175955	0.0229679
2:p	0.0112793	0.9038122E-003	0.0096386	0.0131955
3:p	0.0292179	0.0018259	0.0258440	0.0330172
4:p	0.0110034	0.8888176E-003	0.0093910	0.0128891
5:p	0.0101909	0.8503655E-003	0.0086522	0.0119999
6:p	0.1497040	0.0078111	0.1350302	0.1656670
7:p	0.0591081	0.0038653	0.0519718	0.0671549
8:N_m	10105.707	506.86625	9176.6962	11167.198
9:N_f	10823.240	540.87038	9831.6604	11955.671
10:N_j	705.64357	55.596947	607.59203	826.49940

2002 Real Function Parameters of best model {p(g,t)=c(g,t)}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.0271286	0.0036307	0.0208509	0.0352284
2:p	0.0271286	0.0036307	0.0208509	0.0352284
3:p	0.0130524	0.0021874	0.0093920	0.0181132
4:p	0.0181710	0.0027294	0.0135271	0.0243698
5:p	0.0443083	0.0053429	0.0349398	0.0560430
6:p	0.1059050	0.0115539	0.0852995	0.1307764
7:p	0.1073259	0.0129463	0.0844625	0.1354626
8:p	0.0084352	0.0015084	0.0059385	0.0119690
9:p	0.0173305	0.0026080	0.0128948	0.0232561
10:p	0.0096621	0.0016643	0.0068903	0.0135338
11:p	0.0122694	0.0019896	0.0089236	0.0168481
12:p	0.0347109	0.0047275	0.0265473	0.0452681
13:p	0.0984715	0.0127336	0.0761770	0.1263982
14:p	0.0853894	0.0122774	0.0642000	0.1127300
15:p	0.0304536	0.0136863	0.0125037	0.0722855
16:p	0.0055371	0.0032207	0.0017662	0.0172199
17:p	0.0018457	0.0015126	0.3697E-003	0.0091595
18:p	0.0027685	0.0019674	0.6863E-003	0.0110965
19:p	0.0036982	0.0024033	0.0010326	0.0131542

20:p	0.0602063	0.0261280	0.0252596	0.1367202
21:p	0.0473084	0.0220233	0.0187002	0.1145727
22:N_m	3907.3162	365.13974	3280.1024	4721.3191
23:N_f	6520.3058	770.09256	5226.1390	8273.0718
24:N_j	1083.6184	450.18288	532.62125	2440.7250

2003 Real Function Parameters of best model {p(g,t)=c(g,t)}

			95% Confidence Interval	
Parameter	Estimate	Standard Error	Lower	Upper
1:p	0.0230860	0.0020208	0.0194400	0.0273968
2:p	0.0102453	0.0010925	0.0083113	0.0126237
3:p	0.1131697	0.0082488	0.0979814	0.1303720
4:p	0.0431275	0.0035050	0.0367568	0.0505443
5:p	0.0232968	0.0021500	0.0194347	0.0279045
6:p	0.0259020	0.0024917	0.0214415	0.0312607
7:p	0.0127606	0.0014572	0.0101985	0.0159559
8:p	0.0851820	0.0069736	0.0724711	0.0998821
9:p	0.0724885	0.0062755	0.0611101	0.0857918
10:p	0.0561871	0.0053376	0.0465962	0.0676120
11:p	0.0457965	0.0224769	0.0172117	0.1162394
12:p	0.0034176	0.0022305	0.9491E-003	0.0122269
13:p	0.0020506	0.0015335	0.4728E-003	0.0088471
14:p	0.0225560	0.0114184	0.0082929	0.0598699
15:p	0.0272728	0.0139642	0.0098938	0.0729308
16:N_m	6944.295	479.687800	6080.41515	7966.22144
17:N_f	4980.791	375.132065	4313.15051	5789.12743
18:N_j	693.913	330.350749	304.840416	1721.66964

2009 Real Function Parameters of best model {p(g,t)=c(g,t)}

			95% Confidence Interval	
Parameter	Estimate	Standard Error	Lower	Upper
1:p	0.0276041	0.0030532	0.0222103	0.0342620
2:p	0.0542564	0.0048525	0.0454945	0.0645916
3:p	0.0613590	0.0053877	0.0516105	0.0728076
4:p	0.0936793	0.0078168	0.0794411	0.1101642

5:p	0.3346224	0.0258227	0.2860450	0.3869780
6:p	0.0330897	0.0032175	0.0273319	0.0400105
7:p	0.0674520	0.0053066	0.0577660	0.0786266
8:p	0.0575590	0.0047526	0.0489214	0.0676132
9:p	0.0731203	0.0058051	0.0625264	0.0853456
10:p	0.2167056	0.0150444	0.1886688	0.2476370
11:p	0.0184154	0.0044417	0.0114575	0.0294727
12:p	0.0258811	0.0058090	0.0166324	0.0400631
13:p	0.0269167	0.0060043	0.0173437	0.0415502
14:p	0.0205289	0.0048543	0.0128896	0.0325465
15:p	0.1478695	0.0281150	0.1007663	0.2118049
16:N_f	4202.2703	260.77204	3747.9100	4775.7616
17:N_m	4714.4645	269.04124	4233.1210	5291.2675
18:N_j	2009.1883	357.41223	1450.5345	2879.4580

2010 Real Function Parameters of best model {p(*),s(g,t),b(g,t)}

			95% Confidence Interval	
Parameter	Estimate	Standard Error	Lower	Upper
1:p	0.0890119	0.0047234	0.0801781	0.0987146
2:Phi	0.7250450	0.0695480	0.5709799	0.8393503
3:Phi	1.0000000	0.0000000	1.0000000	1.0000000
4:Phi	1.0000000	0.0000000	1.0000000	1.0000000
5:Phi	0.8805597	0.0977802	0.5437717	0.9785416
6:Phi	0.8650139	0.1158932	0.4780655	0.9781816
7:Phi	1.0000000	0.0000000	1.0000000	1.0000000
8:Phi	1.0000000	0.0000000	1.0000000	1.0000000
9:Phi	1.0000000	0.0000000	1.0000000	1.0000000
10:Phi	1.0000000	0.0000000	1.0000000	1.0000000
11:Phi	1.0000000	0.0000000	1.0000000	1.0000000
12:Phi	0.7372080	0.0609597	0.6022323	0.8386530
13:Phi	1.0000000	0.0000000	1.0000000	1.0000000
14:Phi	1.0000000	0.0000000	1.0000000	1.0000000
15:Phi	1.0000000	0.0000000	1.0000000	1.0000000
16:Phi	1.0000000	0.0000000	1.0000000	1.0000000
17:Phi	1.0000000	0.0000000	1.0000000	1.0000000
18:Phi	1.0000000	0.0000000	1.0000000	1.0000000
19:Phi	0.6604246	0.0603354	0.5344140	0.7671879
20:Phi	0.3381706	0.0774705	0.2058874	0.5017453

21:Phi	1.0000000	0.0000000	1.0000000	1.0000000
22:Phi	1.0000000	0.0000000	1.0000000	1.0000000
23:Phi	0.5312355	0.1270843	0.2941860	0.7549796
24:Phi	1.0000000	0.0000000	1.0000000	1.0000000
25:Phi	0.2367669	0.0502641	0.1524307	0.3485742
26:Phi	1.0000000	0.0000000	1.0000000	1.0000000
27:Phi	0.9999998	0.0000000	0.9999998	0.9999998
28:Phi	1.0000000	0.0000000	1.0000000	1.0000000
29:Phi	0.6890702	0.2179901	0.2317570	0.9421313
30:Phi	1.0000000	0.0000000	1.0000000	1.0000000
31:Phi	1.0000000	0.0000000	1.0000000	1.0000000
32:pent	0.508E-035	0.4053E-036	0.4288E-035	0.5877846E-035
33:pent	0.689E-005	0.0011800	0.1702E-150	1.0000000
34:pent	0.0958351	0.0222619	0.0602032	0.1492078
35:pent	0.891E-039	0.7111E-040	0.75244E-039	0.1031233E-038
36:pent	0.1518397	0.0323757	0.0985911	0.2266174
37:pent	0.1926033	0.0319934	0.1374747	0.2630957
38:pent	0.1720E-005	0.1932E-003	0.41419E-101	1.0000000
39:pent	0.9785E-047	0.7803E-048	0.82562E-047	0.1131521E-046
40:pent	0.3193959	0.0268896	0.2691388	0.3742324
41:pent	0.2403E-005	0.4614E-003	0.91398E-169	1.0000000
42:pent	0.1858E-035	0.1247E-036	0.16138E-035	0.2102932E-035
43:pent	0.7372E-008	0.3142E-005	0.61515E-005	0.6166302E-005
44:pent	0.1904564	0.0218992	0.1511726	0.2370971
45:pent	0.3848E-043	0.2583E-044	0.33419E-043	0.4354599E-043
46:pent	0.1367E-038	0.9180E-040	0.11876E-038	0.1547514E-038
47:pent	0.2025527	0.0256024	0.1569519	0.2573578
48:pent	0.3766E-223	0.0000000	0.3766E-223	0.3766701E-223
49:pent	0.3030E-035	0.2034E-036	0.2632E-035	0.3429678E-035
50:pent	0.2971968	0.0228764	0.2543870	0.3438881
51:pent	0.2369E-097	0.1590E-098	0.20576E-097	0.2681237E-097
52:pent	0.2209E-067	0.2861E-068	0.16482E-067	0.2770085E-067
53:pent	0.6119E-007	0.5644E-004	0.43602E-224	1.0000000
54:pent	0.2239562	0.0465340	0.1458488	0.3278383
55:pent	0.2143E-066	0.2776E-067	0.1599E-066	0.2687589E-066
56:pent	0.3481E-009	0.1916E-005	0.3755E-005	0.3755829E-005
57:pent	0.1674E-037	0.2168E-038	0.12489E-037	0.2099067E-037
58:pent	0.1512E-102	0.1959E-103	0.11284E-102	0.1896431E-102
59:pent	0.9243E-151	0.1197E-151	0.68968E-151	0.1159092E-150
60:pent	0.5170609	0.0414573	0.4360684	0.5971669
61:pent	0.2553E-304	0.0000000	0.2553E-304	0.2553487E-304
62:N	3972.2296	189.4372337	3626.360626	4370.452846
63:N	3612.8432	180.2334058	3284.22877	3992.224406

64:N 773.3108 66.99224706 655.3404128 919.1488068

Note 1: Survival probabilities (s) indicated as "phi" and entrance probabilities (b) indicated as "pent".

2010 Derived abundance parameters and gross population estimates of best model {p(*),s(g t),b(g t)}

Grp.	Occ.	N-hat	Standard Error	95% Confidence Interval Lower	Upper
1	1	1132.1785	108.05810	920.38462	1343.9724
1	2	819.43025	76.096327	670.28144	968.57905
1	3	806.46275	76.105267	657.29642	955.62907
1	4	1257.9635	110.71755	1040.9571	1474.9699
1	5	1020.5366	109.91105	805.11093	1235.9622
1	6	1563.5287	148.67097	1272.1336	1854.9238
1	7	2346.9263	143.71609	2065.2427	2628.6098
1	8	2145.9344	143.71504	1864.2529	2427.6159
1	9	1955.9343	143.71494	1674.2531	2237.6156
1	10	3335.6808	209.33948	2925.3754	3745.9862
1	11	3037.6921	209.33923	2627.3872	3447.9970
2	1	1426.7359	118.95141	1193.5912	1659.8807
2	2	1051.0640	91.410604	871.89920	1230.2288
2	3	1051.0640	91.410611	871.89922	1230.2288
2	4	1928.1983	114.66925	1703.4466	2152.9500
2	5	1902.1983	114.66925	1677.4466	2126.9500
2	6	1887.1983	114.66925	1662.4466	2111.9500
2	7	2725.0411	148.16026	2434.6470	3015.4352
2	8	2539.0411	148.16026	2248.6470	2829.4352
2	9	1577.7816	154.33210	1275.2906	1880.2725
2	10	1869.1384	138.17438	1598.3167	2139.9602
2	11	1697.1384	138.17438	1426.3167	1967.9602
3	1	305.65661	42.046680	223.24512	388.06811
3	2	305.65661	42.046680	223.24512	388.06811
3	3	162.37571	38.489176	86.936925	237.81450
3	4	426.69325	63.502750	302.22786	551.15864
3	5	101.02683	17.542213	66.644091	135.40957
3	6	101.02683	17.542210	66.644096	135.40956
3	7	100.02681	17.542201	65.644098	134.40953
3	8	99.026812	17.542201	64.644098	133.40953
3	9	66.169211	21.349215	24.324749	108.01367
3	10	675.41466	68.020827	542.09384	808.73549

3	11	619.41466	68.020827	486.09384	752.73549

				95% Confidence Interval	
Grp.	Occ.	N*-hat	Standard Error	Lower	Upper
1	0	4711.2262	224.68028	4301.0115	5183.5352
2	0	4605.4329	229.75059	4186.5352	5089.0450
3	0	1180.2197	102.24294	1000.1744	1402.7963

Note 1: Group 1: Females; Group 2: Males; Group 3: Jacks

2011 Real Function Parameters of best model {p(g),s(g,t),b(g,t)}

			95% Confidence Interval	
Parameter	Estimate	Standard Error	Lower	Upper
1:Phi	0.8187871	0.1500760	0.3835940	0.9704198
2:Phi	0.9999993	0.2251E-003	0.1734E-276	1.0000000
3:Phi	0.9999930	0.8954E-003	0.3608E-104	1.0000000
4:Phi	0.7193718	0.1422987	0.3916885	0.9107572
5:Phi	0.1184846	0.0187690	0.0863473	0.1604819
6:Phi	0.9999995	0.0000000	0.9999995	0.9999995
7:Phi	0.6507137	0.1494075	0.3393391	0.8710862
8:Phi	0.7507498	0.1302250	0.4350192	0.9217693
9:Phi	0.6988497	0.0496884	0.5936508	0.7866038
10:Phi	0.4894431	0.1108950	0.2865830	0.6958410
11:Phi	0.3621E-009	0.3411E-006	0.6683E-006	0.6690992E-006
12:Phi	1.0000000	0.0000000	1.0000000	1.0000000
13:Phi	0.3937962	0.4395308	0.0172911	0.9599731
14:Phi	0.2513178	0.2795315	0.0179258	0.8605942
15:Phi	0.1910451	0.0687088	0.0899197	0.3608095
16:Phi	0.9999999	0.8246E-004	0.45407E-301	1.0000000
17:Phi	0.7529E-010	0.0000000	0.7529E-010	0.7529687E-010
18:Phi	0.8742206	0.0000000	0.8742206	0.8742206
19:p	0.1390110	0.0167550	0.1093002	0.1752094
20:p	0.1860167	0.0238067	0.1437766	0.2372283
21:p	0.1424525	0.0935830	0.0356892	0.4271303
22:pent	0.1278042	0.0256726	0.0853391	0.1870782
23:pent	0.2950601	0.0395720	0.2237711	0.3780007
24:pent	0.1222871	0.0383073	0.0647382	0.2190141
25:pent	0.3185412	0.0538362	0.2232921	0.4318310
26:pent	0.1543E-006	0.0000000	0.1543E-006	0.1543743E-006

27:pent	0.0247741	0.0143151	0.0078905	0.0750515
28:pent	0.1150888	0.0199985	0.0813116	0.1604467
29:pent	0.4662919	0.0293431	0.4094747	0.5239973
30:pent	0.2955E-005	0.2876E-003	0.4223E-088	1.0000000
31:pent	0.2629520	0.0297182	0.2089570	0.3251642
32:pent	0.0300200	0.0067577	0.0192601	0.0465062
33:pent	0.0298735	0.0101862	0.0152268	0.0577821
34:pent	0.1404217	0.0761597	0.0452829	0.3600609
35:pent	0.4708776	0.0734645	0.3330230	0.6133228
36:pent	0.8170E-009	0.0000000	0.8170E-009	0.8170272E-009
37:pent	0.1893523	0.0554937	0.1031395	0.3217741
38:pent	0.3051E-012	0.0000000	0.3051E-012	0.3051224E-012
39:pent	0.0249091	0.0176167	0.0061270	0.0957216
40:N	4024.9582	347.8203537	3420.824667	4792.183372
41:N	3661.3679	351.1559877	3060.554449	4447.146233
42:N	295.64126	170.1245423	123.2763016	890.9874588

Note 1: Survival probabilities (s) indicated as "phi" and entrance probabilities (b) indicated as "pent".

2011 Derived abundance parameters and gross population estimates of best model {p(g),s(g,t),b(g,t)}

				95% Confidence Interval	
Grp.	Occ.	N-hat	Standard Error	Lower	Upper
1	1	481.94734	82.390265	320.46241	643.43226
1	2	946.86876	137.22667	677.90449	1215.8330
1	3	2221.8566	276.68931	1679.5455	2764.1676
1	4	2584.2589	306.02272	1984.4544	3184.0635
1	5	2993.0674	386.35846	2235.8048	3750.3299
1	6	305.81736	58.297700	191.55386	420.08085
1	7	371.86901	67.709564	239.15826	504.57975
2	1	360.15160	63.454683	235.78041	484.52278
2	2	667.15376	100.51911	470.13631	864.17121
2	3	2254.3838	276.72073	1712.0111	2796.7564
2	4	1476.2499	206.15874	1072.1788	1880.3211
2	5	1601.7517	223.36555	1163.9552	2039.5482
2	6	112.89206	28.499898	57.032254	168.75186
2	7	204.23310	42.291043	121.34265	287.12354
3	1	98.208117	69.582125	38.172850	234.58908
3	2	117.73040	81.661879	42.326882	277.78769
3	3	294.68857	190.72208	79.126717	668.50385

3	4	55.916707	43.895941	30.119340	141.95275
3	5	156.52074	103.95949	47.239871	360.28135
3	6	0.1022E-007	0.0000000	0.1022E-007	0.1022E-007

				95% Confidence Interval	
Grp.	Occ.	N*-hat	Standard Error	Lower	Upper
1	0	4321.1141	373.41293	3672.5285	5144.7916
2	0	3760.5587	360.66922	3143.4685	4567.6247
3	0	562.99303	323.97011	234.75647	1696.7176

Note 1: Group 1: Females; Group 2: Males; Group 3: Jacks

2012 Real Function Parameters of best model {p(g),s(*),b(g,t)}

			95% Confidence Interval	
Parameter	Estimate	Standard Error	Lower	Upper
1:Phi	0.5914912	0.0186959	0.5544038	0.6275654
2:p	0.3680193	0.0449145	0.2851157	0.4595333
3:p	0.3349530	0.0386640	0.2638484	0.4144320
4:p	0.2425276	0.0337780	0.1825370	0.3146455
5:pent	0.0898898	0.0126780	0.0679432	0.1180278
6:pent	0.1377143	0.0159224	0.1093683	0.1719884
7:pent	0.2832150	0.0212978	0.2433869	0.3267460
8:pent	0.2365248	0.0220557	0.1960422	0.2824304
9:pent	0.2026523	0.0209887	0.1646003	0.2469011
10:pent	0.1351E-006	0.1924E-004	0.9344E-128	1.0000000
11:pent	0.0711283	0.0143257	0.0476763	0.1048463
12:pent	0.1471433	0.0188643	0.1138689	0.1880773
13:pent	0.2728272	0.0245153	0.2274929	0.3234134
14:pent	0.1707533	0.0241548	0.1284590	0.2234032
15:pent	0.2686393	0.0227557	0.2264358	0.3155008
16:pent	0.3134E-010	0.1281E-006	0.25121E-006	0.371273E-006
17:pent	0.1013497	0.0166928	0.0729964	0.1390639
18:pent	0.1376812	0.0200055	0.1029425	0.1817675
19:pent	0.1398410	0.0209783	0.1035449	0.1862173
20:pent	0.2486562	0.0253624	0.2023180	0.3015949
21:pent	0.3021303	0.0247682	0.2558951	0.3527589
22:pent	0.2928E-007	0.1211E-004	0.28875E-311	1.0000000

23:N	1901.4645	179.96188	1612.6613	2329.1267
24:N	1545.8238	140.39491	1315.2399	1872.3387
25:N	2109.8485	243.97249	1711.8920	2680.9065

Note 1: Survival probabilities (s) indicated as "phi" and entrance probabilities (b) indicated as "pent".

2012 Derived abundance parameters and gross population estimates of best model {p(g),s(*),b(g,t)}

				95% Confidence Interval	
Grp.	Occ.	N-hat	Standard Error	Lower	Upper
1	1	95.080075	19.703927	56.460377	133.69977
1	2	227.16137	34.425155	159.68807	294.63468
1	3	387.68662	50.439769	288.82467	486.54857
1	4	681.67262	87.633807	509.91036	853.43489
1	5	670.12314	88.075469	497.49522	842.75107
1	6	615.83221	70.302199	478.03990	753.62453
1	7	184.36046	39.722685	106.50399	262.21692
2	1	107.44796	21.614038	65.084448	149.81148
2	2	173.50639	27.632456	119.34678	227.66601
2	3	323.56515	43.665353	237.98105	409.14924
2	4	571.63377	70.588512	433.28029	709.98726
2	5	492.57331	61.187408	372.64598	612.50063
2	6	603.91718	64.761886	476.98388	730.85048
2	7	198.80901	38.070966	124.18992	273.42810
3	1	148.40994	32.074487	85.543942	211.27593
3	2	301.61570	51.648308	200.38501	402.84638
3	3	457.55546	70.166062	320.02997	595.08094
3	4	514.39452	75.918672	365.59392	663.19512
3	5	761.38764	110.13165	545.52961	977.24567
3	6	959.48748	124.33811	715.78478	1203.1902
3	7	378.03897	73.517168	233.94532	522.13262

				95% Confidence Interval	
Grp.	Occ.	N*-hat	Standard Error	Lower	Upper
1	0	2559.4691	248.71996	2071.9780	3046.9602
2	0	2062.7136	186.53713	1697.1008	2428.3264
3	0	2803.0146	319.17312	2177.4353	3428.5940

Note 1: Group 1: Females; Group 2: Males; Group 3: Jacks

2013 Real Function Parameters of best model {p(g,t)=c(g,t)}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:p	0.0281056	0.0024544	0.0236746	0.0333375
2:p	0.0416247	0.0032922	0.0356295	0.0485778
3:p	0.0037948	0.7064E-003	0.0026341	0.0054643
4:p	0.0327383	0.0027452	0.0277644	0.0385678
5:p	0.0399146	0.0032601	0.0339928	0.0468179
6:p	0.1041998	0.0074706	0.0904398	0.1197775
7:p	0.1204341	0.0093909	0.1032073	0.1400871
8:p	0.0177405	0.0022051	0.0138978	0.0226213
9:p	0.0139644	0.0015154	0.0112854	0.0172683
10:p	0.0230717	0.0022279	0.0190856	0.0278665
11:p	0.0019082	0.4310E-003	0.0012254	0.0029703
12:p	0.0252466	0.0023958	0.0209529	0.0303929
13:p	0.0399065	0.0035857	0.0334422	0.0475588
14:p	0.0897031	0.0077052	0.0757032	0.1059952
15:p	0.1165428	0.0107707	0.0970342	0.1393681
16:p	0.0254394	0.0030491	0.0200999	0.0321509
17:p	0.0172277	0.0032973	0.0118258	0.0250345
18:p	0.0399535	0.0062576	0.0293401	0.0541917
19:p	0.0018327	0.8505E-003	0.7376E-003	0.0045463
20:p	0.0117295	0.0025322	0.0076756	0.0178858
21:p	0.0173870	0.0033409	0.0119174	0.0253027
22:p	0.0685197	0.0100946	0.0511906	0.0911514
23:p	0.1600537	0.0233248	0.1194246	0.2111900
24:p	0.0255032	0.0054390	0.0167567	0.038635 7
25:N_m	8432.5002	500.67483	7533.6559	9502.3456
26:N_f	11529.297	866.79979	10000.026	13412.857
27:N_j	2728.1706	342.08488	2166.8610	3524.4550

9.4. Appendix D

Input data and summary statistics of Generalized Linear Models for Atnarko Chinook escapement as response variable

Data used for calibration of the 1990-2013 time series of Atnarko Chinook escapement

Year	Petn_J	Best_J	Petn_FMJ	Best_FMJ	Petn_FM	Best_FM	Carc_FMJ	Broodstock_CPUE
1990							3612	13.3
1991							2769	14.2
1992							6077	22.1
1993							6381	22.8
1994							5262	25.0
1995							3499	40.4
1996							3758	28.2
1997							1843	16.2
1998							2282	22.1
1999							2378	35.3
2000							3496	21.2
2001	725	706	20769	21635	20044	20929	4559	19.5
2002	1701	1084	16352	11511	14651	10427	2216	12.5
2003	1405	694	13433	12619	12027	11925	2124	21.15
2004							1517	27.2
2005							1304	30.05
2006							3070	37.4
2007							651	16.65
2008							431	12
2009	1533	2009	10764	10926	9231	8917	2624	17
2010	1839	1180	11037	10497	9198	9317	1023	26.5
2011	450	563	9555	8645	9105	8082	775	10.5
2012	4589	2803	10389	7425	5800	4622	1097	8.8
2013	3253	2728	28313	22690	25060	19962	5186	15.7

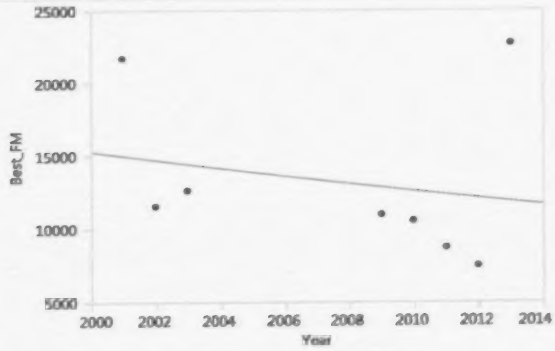
- Petn_J: Petersen estimate of number of Jacks
- Best_J: Best ML model estimate of the number of Jacks
- Petn_FMJ: Petersen estimate of total escapement (females, males and Jacks)
- Best_FMJ: Best ML model estimate of total escapement (females, males and Jacks)
- Petn_FM: Petersen estimate of adult escapement (females and males)
- Best_FMJ: Best ML model estimate of adult escapement (females and males)
- Carc_FMJ: Number of deadpitch carcasses recovered
- Broodstock_CPUE: Broodstock catch per unit effort (catch per net set)

Best ML escapement (including Jacks) as function of Year

Generalized Linear Model Fit

Response: Best_FMJ
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Regression Plot



Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	419.299965	838.5999	1	<.0001 *
Full	7712.31621			
Reduced	8131.61617			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	17252.05	6	<.0001 *
Deviance	15334.59	6	<.0001 *

AICc
15431.032

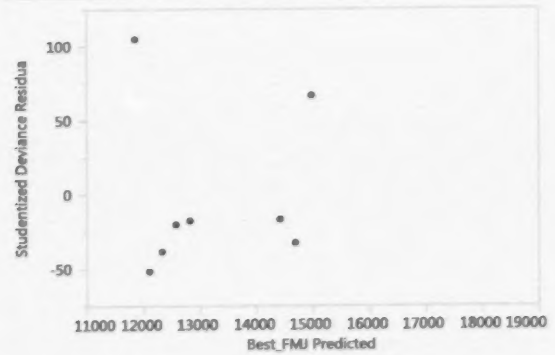
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Year	1	838.59993	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	48.590789	1.3450373	1292.3065	<.0001 *	45.953978	51.226441
Year	-0.019477	0.0006701	838.59993	<.0001 *	-0.020791	-0.018164

Studentized Deviance Residual by Predicted

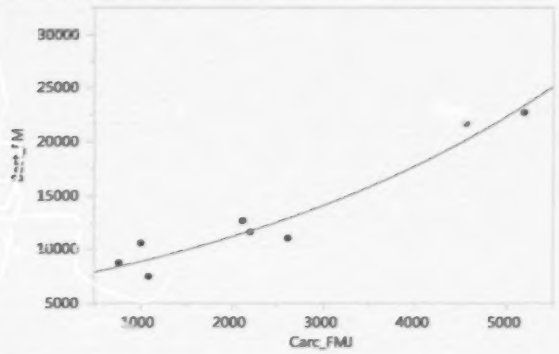


Best ML escapement (including Jacks) as function of the number of carcasses recovered

Generalized Linear Model Fit

Response: Best_FMJ
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Regression Plot



Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	7516.6851	15033.37	1	<.0001 *
Full	614.931078			
Reduced	8131.61617			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	1126.613	6	<.0001 *
Deviance	1139.818	6	<.0001 *

AICc
1236.2622

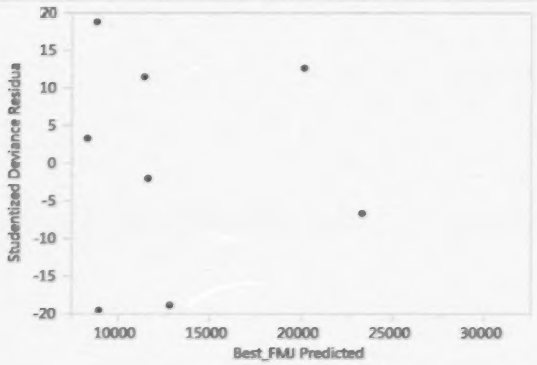
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Carc_FM	1	15033.37	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	8.8546896	0.0064625	594994.71	<.0001 *	8.8420087	8.8673413
Carc_FM	0.0002322	1.8657e-6	15033.37	<.0001 *	0.0002285	0.0002358

Studentized Deviance Residual by Predicted

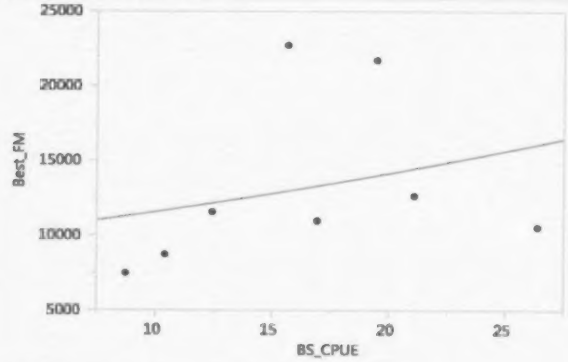


Best ML escapement (including Jacks) as function of broodstock CPUE

Generalized Linear Model Fit

Response: Best_FMJ
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Regression Plot



Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	666.996425	1333.993	1	<.0001 *
Full	7464.61975			
Reduced	8131.61617			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	16209.91	6	<.0001 *
Deviance	14839.20	6	<.0001 *

AICc
14935.639

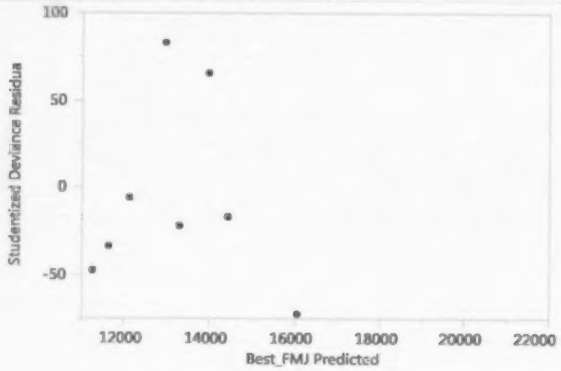
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
BS_CPU	1	1333.9929	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	9.1531082	0.0098814	440736.94	<.0001 *	9.1337273	9.1724618
BS_CPU	0.020185	0.0005504	1333.9929	<.0001 *	0.0191061	0.0212635

Studentized Deviance Residual by Predicted



Best ML escapement (including Jacks) as function of carcasses recovered and broodstock CPUE

Generalized Linear Model Fit

Response: Best_FMJ
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	7808.42079	15616.84	2	<.0001 *
Full	323.195381			
Reduced	8131.61617			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	543.5180	5	<.0001 *
Deviance	556.3468	5	<.0001 *

AICc
658.3908

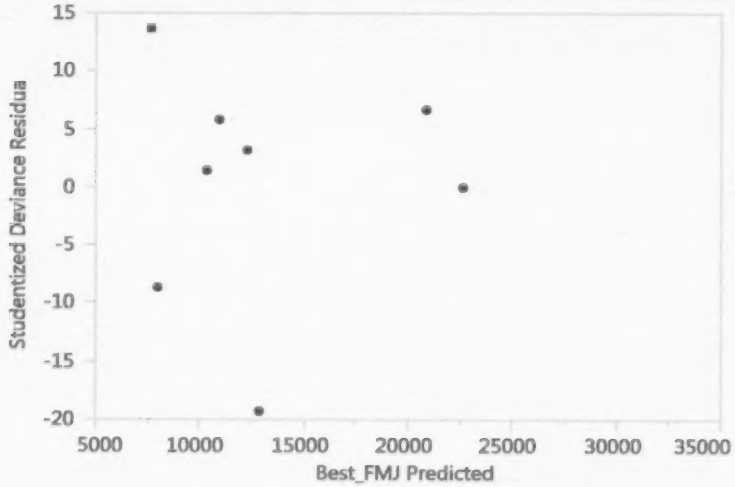
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Carc_FM	1	14282.849	<.0001 *
BS_CPU	1	583.47139	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	8.6033018	0.0124831	205130.98	<.0001 *	8.5787987	8.6277316
Carc_FM	0.0002277	1.8776e-6	14282.849	<.0001 *	0.000224	0.0002314
BS_CPU	0.0156963	0.0006465	583.47139	<.0001 *	0.0144287	0.016963

Studentized Deviance Residual by Predicted



Best ML escapement (including Jacks) as function of carcasses recovered and year

Generalized Linear Model Fit

Response: Best_FMJ
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	7615.47553	15230.95	2	<.0001 *
Full	516.140647			
Reduced	8131.61617			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	944.0309	5	<.0001 *
Deviance	942.2373	5	<.0001 *

AICc
1044.2813

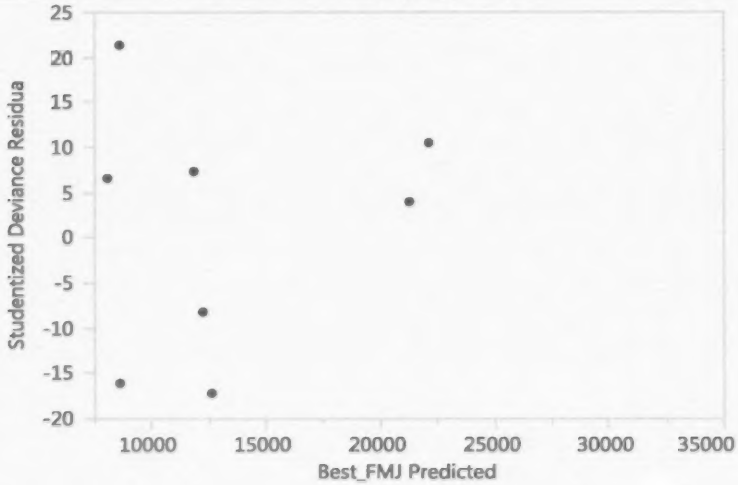
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Carc_FM	1	14392.351	<.0001 *
Year	1	197.58086	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	26.60865	1.2619361	443.2883	<.0001 *	24.135043	29.081758
Carc_FM	0.0002313	1.8855e-6	14392.351	<.0001 *	0.0002276	0.000235
Year	-0.008843	0.0006286	197.58086	<.0001 *	-0.010075	-0.007611

Studentized Deviance Residual by Predicted



Best ML escapement (including Jacks) as function of broodstock CPUE and year

Generalized Linear Model Fit

Response: Best_FMJ
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	882.654527	1765.309	2	<.0001 *
Full	7248.96165			
Reduced	8131.61617			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	16304.89	5	<.0001 *
Deviance	14407.88	5	<.0001 *

AICc
14509.923

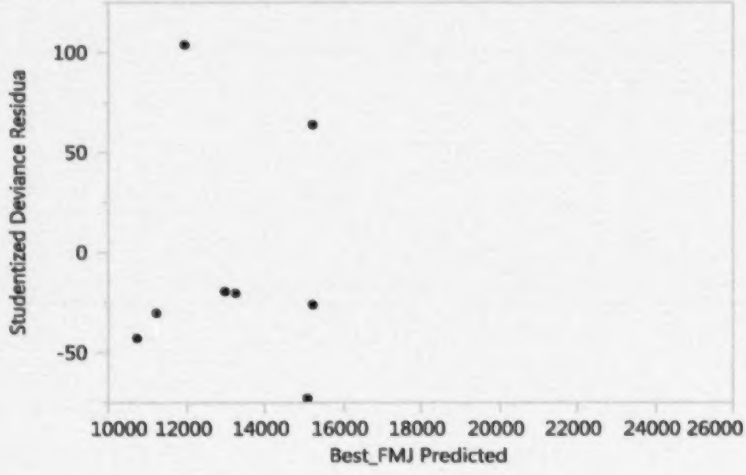
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
BS_CPU	1	926.70912	<.0001 *
Year	1	431.3162	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	38.177978	1.3931219	744.52546	<.0001 *	35.44675	40.907702
BS_CPU	0.0175695	0.0005727	926.70912	<.0001 *	0.0164465	0.0186914
Year	-0.014437	0.000693	431.3162	<.0001 *	-0.015795	-0.013078

Studentized Deviance Residual by Predicted



Best ML escapement (including Jacks) as function of carcasses recovered, broodstock CPUE and year

Generalized Linear Model Fit

Response: Best_FMJ
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	7835.89178	15671.78	3	<.0001 *
Full	295.72439			
Reduced	8131.61617			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	492.0930	4	<.0001 *
Deviance	501.4048	4	<.0001 *

AICc
612.7821

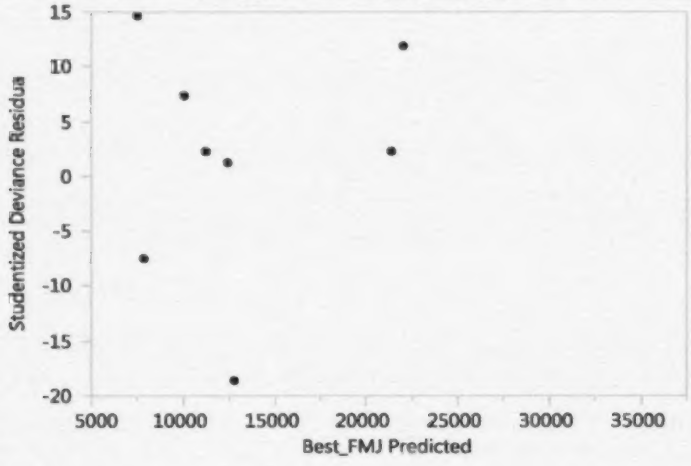
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Carc_FM	1	13906.475	<.0001 *
BS_CPU	1	440.83251	<.0001 *
Year	1	54.94198	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	18.419389	1.3235788	193.21133	<.0001 *	15.824839	21.013188
Carc_FM	0.0002274	1.8886e-6	13906.475	<.0001 *	0.0002237	0.0002311
BS_CPU	0.0143065	0.0006762	440.83251	<.0001 *	0.0129803	0.0156309
Year	-0.004878	0.0006577	54.94198	<.0001 *	-0.006167	-0.003589

Studentized Deviance Residual by Predicted

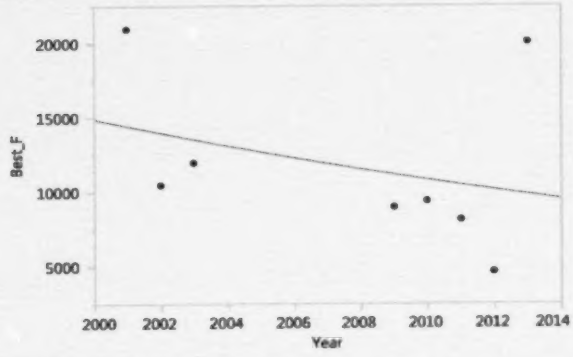


Best ML escapement (excluding Jacks) as function of year

Generalized Linear Model Fit

Response: Best_FM
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Regression Plot



Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	1022.34509	2044.690	1	<.0001 *
Full	8474.36056			
Reduced	9496.70566			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	18735.33	6	<.0001 *
Deviance	16859.86	6	<.0001 *

AICc
16955.121

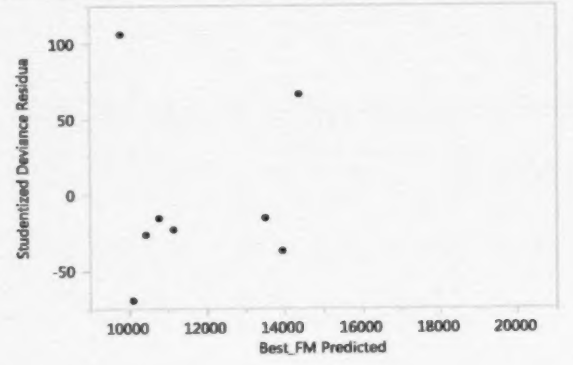
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Year	1	2044.6902	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	73.857919	1.4197469	2677.4818	<.0001 *	71.074911	76.640234
Year	-0.032125	0.0007074	2044.6902	<.0001 *	-0.033511	-0.030738

Studentized Deviance Residual by Predicted

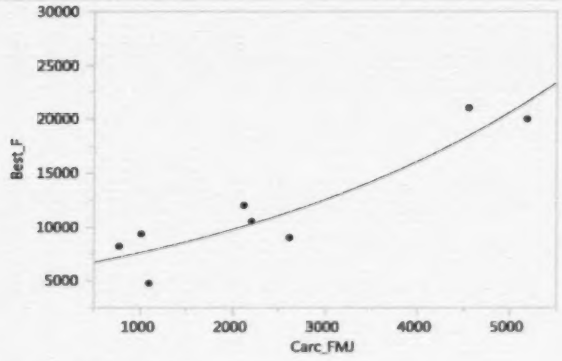


Best ML escapement (excluding Jacks) as function of carcasses recovered

Generalized Linear Model Fit

Response: Best_FM
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Regression Plot



Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	7797.94387	15595.89	1	<.0001 *
Full	1698.76179			
Reduced	9496.70566			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	3112.513	6	<.0001 *
Deviance	3308.660	6	<.0001 *

AICc
3403.9236

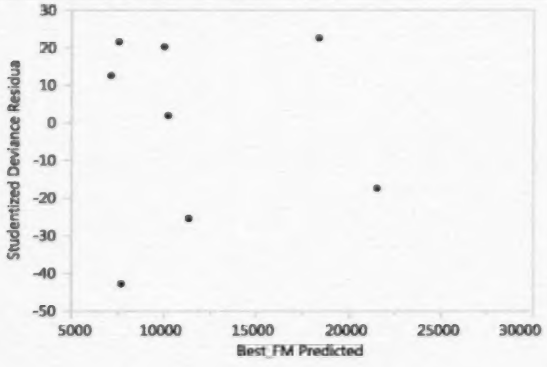
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Carc_FM	1	15595.888	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	8.6813647	0.0069347	503286.9	<.0001 *	8.6677559	8.6949396
Carc_FM	0.0002503	1.9769e-6	15595.888	<.0001 *	0.0002464	0.0002541

Studentized Deviance Residual by Predicted

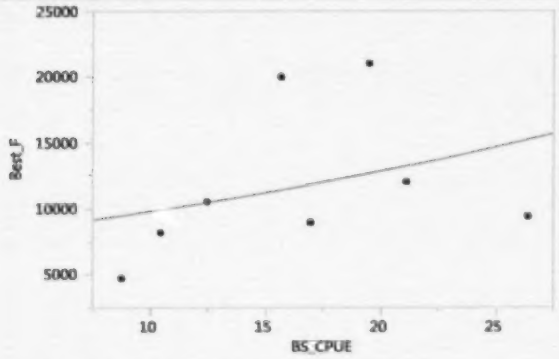


Best ML escapement (excluding Jacks) as function of broodstock CPUE

Generalized Linear Model Fit

Response: Best_FM
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Regression Plot



Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	1066.2521	2132.504	1	<.0001 *
Full	8430.45356			
Reduced	9496.70566			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	17805.76	6	<.0001 *
Deviance	16772.04	6	<.0001 *

AICc
16867.307

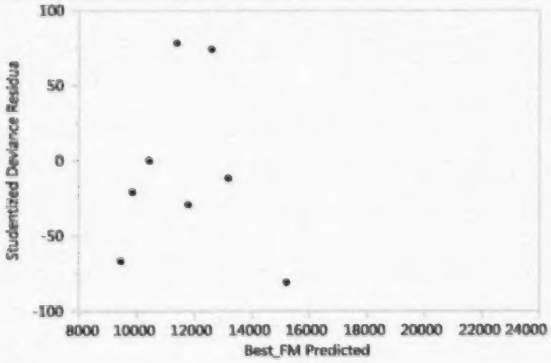
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
BS_CPU	1	2132.5042	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	8.9184082	0.010567	369013.64	<.0001 *	8.8976811	8.9391029
BS_CPU	0.0269971	0.0005818	2132.5042	<.0001 *	0.0258566	0.0281372

Studentized Deviance Residual by Predicted



Best ML escapement (excluding Jacks) as function of carcasses recovered and broodstock CPUE

Generalized Linear Model Fit

Response: Best_FM
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	8440.72409	16881.45	2	<.0001 *
Full	1055.98157			
Reduced	9496.70566			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	1991.662	5	<.0001 *
Deviance	2023.100	5	<.0001 *

AICc
2123.9631

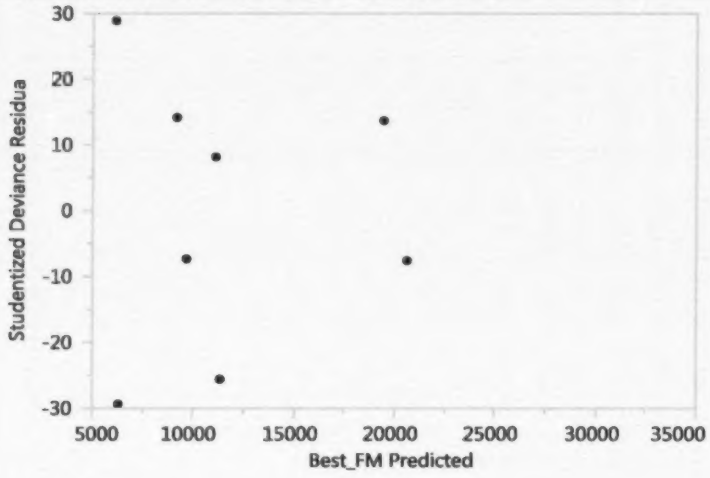
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Carc_FM	1	14748.944	<.0001 *
BS_CPU	1	1285.5604	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	8.2740639	0.0137309	160461.07	<.0001 *	8.2471065	8.3009307
Carc_FM	0.0002449	1.9899e-6	14748.944	<.0001 *	0.000241	0.0002488
BS_CPU	0.0249394	0.0006915	1285.5604	<.0001 *	0.0235837	0.0262945

Studentized Deviance Residual by Predicted



Best ML escapement (excluding Jacks) as function of carcasses recovered and year

Generalized Linear Model Fit

Response: Best_FM
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	8238.43327	16476.87	2	<.0001 *
Full	1258.27239			
Reduced	9496.70566			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	2351.485	5	<.0001 *
Deviance	2427.681	5	<.0001 *

AICc
2528.5448

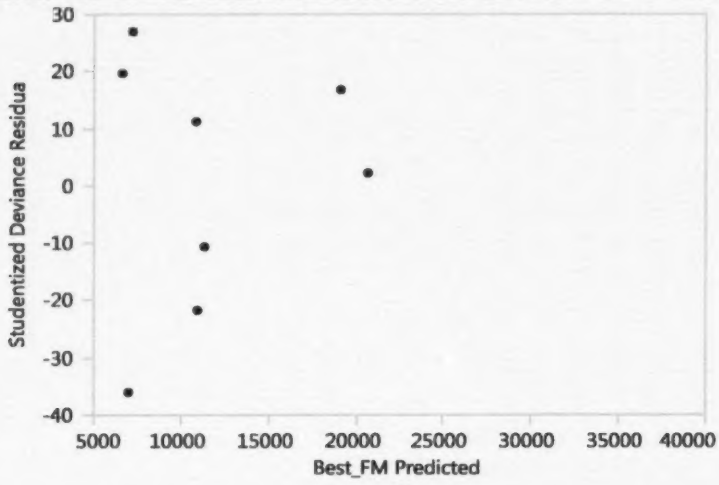
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Carc_FM	1	14432.176	<.0001 *
Year	1	880.9788	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	48.138566	1.3283937	1310.2171	<.0001 *	45.534975	50.742202
Carc_FM	0.0002484	2.0227e-6	14432.176	<.0001 *	0.0002445	0.0002524
Year	-0.019655	0.0006617	880.9788	<.0001 *	-0.020952	-0.018358

Studentized Deviance Residual by Predicted



Best ML escapement (excluding Jacks) as function of broodstock CPUE and year

Generalized Linear Model Fit

Response: Best_FM
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	1696.72769	3393.455	2	<.0001 *
Full	7799.97797			
Reduced	9496.70566			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	17534.66	5	<.0001 *
Deviance	15511.09	5	<.0001 *

AICc
15611.956

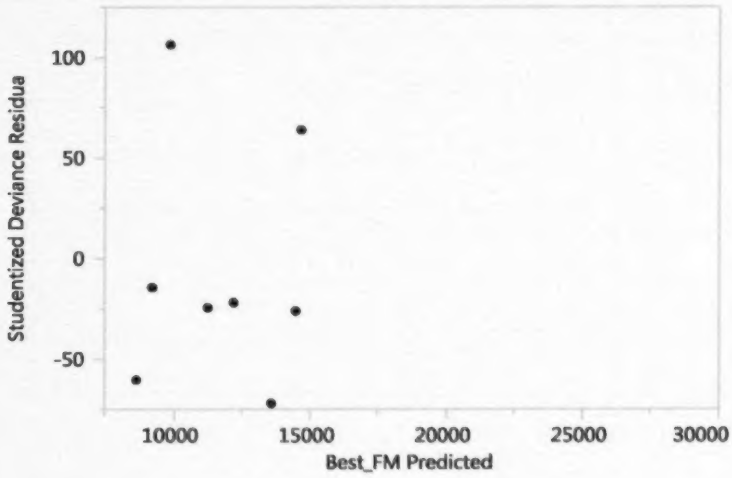
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
BS_CPU	1	1348.7652	<.0001 *
Year	1	1260.9512	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	61.260801	1.4675351	1723.9178	<.0001 *	58.383925	64.136574
BS_CPU	0.0226296	0.0006107	1348.7652	<.0001 *	0.0214321	0.0238261
Year	-0.02604	0.0007301	1260.9512	<.0001 *	-0.02747	-0.024608

Studentized Deviance Residual by Predicted



Best ML escapement (excluding Jacks) as function of carcasses recovered, broodstock CPUE and year

Generalized Linear Model Fit

Response: Best_FM
Distribution: Poisson
Link: Log
Estimation Method: Maximum Likelihood
Observations (or Sum Wgts) = 8

Whole Model Test

Model	-LogLikelihood	L-R ChiSquare	DF	Prob>ChiSq
Differenc	8646.5697	17293.14	3	<.0001 *
Full	850.135955			
Reduced	9496.70566			

Goodness Of Fit Statistic	ChiSquare	DF	Prob>ChiSq
Pearson	1613.736	4	<.0001 *
Deviance	1611.408	4	<.0001 *

AICc
1721.6052

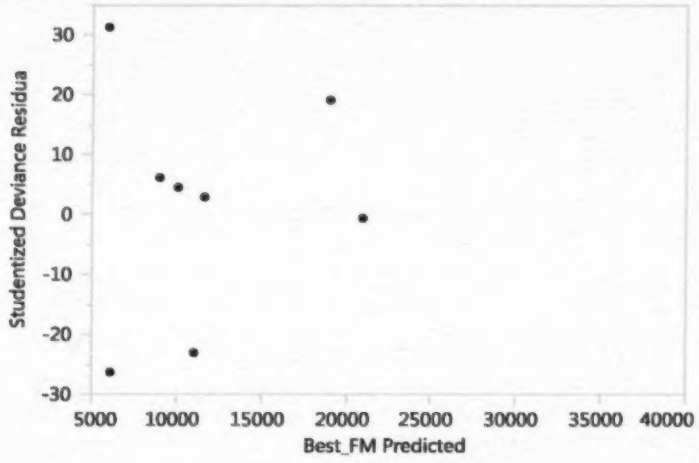
Effect Tests

Source	DF	L-R ChiSquare	Prob>ChiSq
Carc_FM	1	13899.684	<.0001 *
BS_CPU	1	816.27287	<.0001 *
Year	1	411.69123	<.0001 *

Parameter Estimates

Term	Estimate	Std Error	L-R ChiSquare	Prob>ChiSq	Lower CL	Upper CL
Intercep	36.554184	1.3927421	687.26623	<.0001 *	33.824333	39.283799
Carc_FM	0.0002435	2.0223e-6	13899.684	<.0001 *	0.0002396	0.0002475
BS_CPU	0.0209815	0.0007274	816.27287	<.0001 *	0.019555	0.0224064
Year	-0.014054	0.0006921	411.69123	<.0001 *	-0.01541	-0.012697

Studentized Deviance Residual by Predicted



This is the end of this report.

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